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RESULT
                                                                                               September 10, 2001, 14:01:21; Search time 72.54 Seconds (without alignments) 32.830 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                       425026
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                  425026 seqs, 132305027 residues
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Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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103
1 GIVPFRSFWQQRLHDSQH 18
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sp_bacteria:*
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sp_fungi:*
sp_human:*
sp_mammal:*
sp_mhc:*
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sp_plant:*
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sp_punclassified:*
sp_unclassified:*
sp_voertebrate:*
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Maximum DB seq length: 200000000
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Perfect score:
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Description	O94994 homo sapien	Q9r0w4 rattus norv	Q9qw28 rattus sp.	09ttt6 oryctolagus	Q9n175 ovis aries	097604 canis famil	Q9n176 ovis aries	Q9wtk6 cavia porce	Q9pu92 cyprinus ca	Q9jjy7 rattus norv	Q9tux8 canis famil	077104 manduca sex	Q9vkp8 drosophila	Q42697 chlamydomon	Q9s9e0 chlamydomon	Q41641 volvox cart	Q9n127 ovis aries	Q9kay1 bacillus ha	032214 bacillus su
ID	094994	Q9R0W4	Q9QW28	Q9TTT6	Q9N175	097604	971N6Q	O9WTK6	Q9PU92	711160	Q9TUX8	077104	Q9VKP8	042697	Q9S9E0	041641	Q9N127	Q9KAY1	032214
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Query Match Length DB	1114	1147	1147	82	945	1154	366	1206	1127	306	1205	1206	1349	255	320	346	146	267	605
Query Match	96.1	96.1	96.1	87.4	86.4	86.4	73.8	72.8	71.8	70.9	68.8	54.4	54.4	49.5	49.5	49.5	47.6	47.6	46.6
Score	66	66	66	90	83	83	97	75	74	73	7.1	26	26	21	21	51	49	49	48

3 6 7 7 8 8 8 111 111 112 114 116 116 116 116

	Q91334 pseudomonas Q18648 caenorhabdi Q9pd80 xylella fas
2 Q9KF76 2 Q9KUX4 10 024425 10 024425 11 096560 2 Q9UD8 2 Q9UD8 2 Q9UD8 10 Q9FWM 10 Q9FWM 10 Q9SWM 10	2 Q91334 5 Q18648 2 Q9PD80
6014 6014 7059 7059 8030 6024 7044 7044 7044 7044 8030 8030 8030 8030 8030 8030 8030 8	217 326 612
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ALIGNMENTS

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3 2	FRELIMINARI; FRI;
) E	01-MAY-1999 (TrEMBLrel. 10, Created)
ΕĪ	(TrEMBLrel. 10,
DŢ	(TrEMBLrel.
DE	INDUCIBLE NITRIC OXIDE SYNTHASE.
ВN	INOS.
SO	Homo sapiens (Human).
ပ္ပ	Chordata;
ပ္ပ	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
×o	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Ogawa Y., Nishijima S., Goto M., Ida M.;
RT	"Cloning and characterization of a novel splice valiant of human
RT	inducible nitric oxide synthase.";
RL	Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
O.R.	EMBL; AB022318; BAA37123.1;
E,	HSSP; P35228; 4NOS.
DR	
DR.	
D.	InterPro; IPR001709;
O.R	InterPro; IPR003097;
DR DR	PF00175;
DR	Pfam; PF00667; FAD_binding; 1.
DR	PRINTS; PR00369; FLAVODOXIN.
DR	FPNCR.
Q	SEQUENCE 1114 AA; 126748 MW; C1F9624774435571 CRC64;
28	Query Match 96.1%; Score 99; DB 4; Length 1114; Best Local Similarity 94.4%; Pred NO 2.7e-08;
Ma	vative 0
οy	1 GIVPFRSFWQQRLHDSQH 18
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g	946 GIAPFRSFWQQRLHDSQH 963

SUMMARIES

Result No. RESULT 2

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Query Match
Best Local Similarity
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                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                           STRAIN-WISTAR KYOTO;
MEDLINE-9932503; PubMed-10395902;
MEDLINE-9932503; PubMed-10395902;
Medianen R.A., Vartiainen N., Koistinaho J.;
"Molecular cloning and characterization of the rat inducible nitric oxide synthase (INOS) gene.";
Gene 224:297-305 (1999).
Gene 124:297-305 (1999).
EMBL; AJ230463; CAB46089.1; ---
EMBL; AJ230464; CAB46089.1; JOINED.
EMBL; AJ230465; CAB46089.1; JOINED.
EMBL; AJ230465; CAB46089.1; JOINED.
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Pred. No. 2.7e-08;
^. Wismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E76B3F8407D54CF6 CRC64
                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INDUCIBLE NITRIC OXIDE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
         PRT; 1147 AA
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Pfam; PF00175; oxidored_fad; 1.
Pfam; PF00667; FAL_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
SEQUENCE 1147 AA; 130613 Mar.
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94.4%;
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CAB46089.1;
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CAB46089.1;
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                                                                                                                                                                                                                                                                             CAB46089.
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Best Local Similarity 94.4
Matches 17; Conservative
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         PRELIMINARY;
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InterPro; IPR001433
                                                                                              NCBI_TaxID=10116;
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AJ230475;
AJ230476;
AJ230477;
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AJ230487;
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EMBL;
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                                                                                                            Rattus sp. Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukarnyota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shi Y., Pritchard K.A., Baker J.E.; "Chronic myocardial hypoxia increases nitric oxide synthase and decreases caveolin-3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 99; DB 11; Length 1147;
Pred. No. 2.7e-08;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1147 AA; 130625 MW; 2CAFB983E56F651A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
STRAIN-NEW ZEALAND WHITE; TISSUE-KIDNEY;
Tsao L.S., O'Brien W.J.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73244479A4B965F6 CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
INDUCIBLE NITRIC OXIDE SYNTHASE NOS2 (FRAGMENT).
01-MAR-2001 (TrEMBLrel. 16, Last annotation update) CYTOKINE INDUCIBLE NITRIC OXIDE SYNTHASE, INOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
STRAIN-NEW ZEALAND WHITE; TISSUE-HEART MYOCARDIUM;
PubMed-11053770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 90; DB 6;
Pred. No. 5.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Free Radic. Biol. Med. 29:695-703(2000).
EMBL, AF198443; AAF09500.1; -.
EMBL; AF200351; AAC24286.1; -.
INTESP: PO03088; IAMO.
INTERPRO; IPRO01709; -.
PRINTS; PRO0371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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94.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GIVPFRSFWQQRLHDSQH 18
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Best Local Similarity 94.4
Matches 17; Conservative
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PRT;
InterPro; IPR001709; -.
InterPro; IPR003097; -.
Pfam; PF00175; oxidored_fad; 1.
Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00369; FLAVDOXIN.
PRINTS; PR00371; FPNCR.
SEQUENCE 1154 AA; 131709 MW;
                                                                                                   86.4%;
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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264 GIAPFRAFWQERLHD 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                   Query Match
Best Local Similarity
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SEQUENCE
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Q9N176;
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MEDIATR=9841941; PubMed=9746458;
MEDIATR=9841941; PubMed=9746458;
Wang X., McGregor C.G.A., Miller V.M.;
"Induction and cDNA sequence of inducible nitric oxide synthase from canine aortic smooth muscle cells.";
Am. J. Physiol. 275:H1129:H1129(1998).
EMBL; AF077821; AAC78630.1; -.
HSSP; P29477; INOS.
InterPro; IPR001949; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
     Gaps
                                                                                                                                                                 Ovis aries (Sheep).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INDUCIBLE NITRIC OXIDE SYNTHASE.
Canis familiaris (Dog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia: Eutheria, Carnivora, Fissipedia, Canis.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Mershon J.L., Clark K.E.; "Estrogen increases the expression of iNOS in the ovine coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Pred. No. 1.1e-06;
3; Mismatches 1; Indels
    Indels
                                                                                                                                                                                                                                                                            Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF223942; AAF34710.1; -.
InterPro; IPR001094; -.
InterPro; IPR0011094; -.
InterPro; IPR001709; -.
InterPro; IPR003097; -.
Pfam; PF00175; Oxidored_fad; 1.
Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                108001 MW; 9A5ACFD40440A74F CRC64;
                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INDUCIBLE NITRIC OXIDE SYNTHANSE (FRAGMENT).
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                                                                                                   945 AA
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    Mismatches
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Best Local Similarity 77.8%;
Matches 14; Conservative
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                                    31 GIAPFRSFWQQRLHDSEY 48
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                         1 GIVPFRSFWQQRLHDSQH 18
   15; Conservative
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SEQUENCE
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Q9N175;
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Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
NCBL_TaxID=10141;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
Mershon J.L., Clark K.E.;
"Estrogen increases the expression of iNOS in the ovine coronary
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                                                                              Score 89; DB 6; Length 1154;
Pred. No. 1.4e-06;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
1154 AA; 131709 MW; 42CD606E447254CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               artery.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, AR23471; ARF34707.1; ...
InterPro; IPR001433; ...
InterPro; IPR001409; ...
InterPro; IPR00159; ...
Pfam; PF00175; oxidored_fad; 1.
Pfam; PF00677; FAD_binding; 1.
Print; PR00371; FPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 366
366 Aa; 40791 MW; 794B274DA786A4A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ENDOTHELIAL NITRIC OXIDE SYNTHASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.7.07.1999 (TrEMBLrel. 12, Created)
0.1.NOV-1999 (TrEMBLrel. 12, Last sequence update)
0.1.NAR-2001 (TrEMBLrel. 16, Last annotation update)
ENDOTHELIAL NITRIC OXIDE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 76; DB 6; 1
Pred. No. 6.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                    366 AA
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                                                                                                                                      1; Mismatches
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Best Local Similarity
Matches 12; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-HEART
                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
NON_TER
SEQUENCE
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                                                                                                                         09JJY7
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                                                                                              09JJY7
                                                    RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Saeij J.P., Stet R.J., Groeneveld A., Verburg-van Kemenade L.B., Wiegertjes G.F.; "Identification and characterization of a fish inducible nitric oxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyprinus carpio (Common carp).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.

NCBI_TaxID=7962;
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                                                                                                                                                                                                                                                                                                                                                                                                              72.8%; Score 75; DB 11; Length 1206; 80.0%; Pred. No. 0.00033; 1ve 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                     Derst C., Preisig-Mueller R., Rajan S., Daut J.;
"Cloning and sequencing of guinea pig NO synthases.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF146041; AAD29753.1; -.
EMBL; AF146040; AAD29753.1; -.
HSP; P29474; 3NOS.
InterPro; IPR001094; -.
InterPro; IPR001433; -.
InterPro; IPR001709; -.
InterPro; IPR001709; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1127 AA; 127431 MW; 8317FC67C7A3DD9A CRC64;
                                                                                                                                                                                                                                                                                                                                                   EB4E792D3F9503DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INDUCIBLE NITRIC OXIDE SYNTHASE (EC 1.14.13.39).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00175; oxidored_fad; 1.
Pfam; PF0067; FAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
PRODOM; PD002221; -: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 74; DB 13;
Pred. No. 0.00045;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1127 AA
                                                                                                                                                                                                                                                                                                                                                 1206 AA; 133692 MW;
                                                                                                                                                                                                                                                    Pfam; PF00175; oxidored_fad; 1.
Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenetics 0:0-0(0).
EMBL; AJ242906; CAB60197.1; -
HSSP; P29477; 1NOS.
InterPro; IPR001094; -
InterPro; IPR001043; -
InterPro; IPR001522; -
InterPro; IPR001509; -
InterPro; IPR00106; -
InterPro; IPR00106; -
InterPro; IPR003097; -
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.8
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1020 GIAPFRGFWQERLHD 1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GIVPFRSFWQQRLHD 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GIVPFRSFWQQRLHD 15
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Best Local Similarity
Matches 12; Conservi
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthase cDNA.";
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Q9PU92
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                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE-99369487; PubMed-10442857; Schwemmer M., Bassenge E.; "Assembly and characterization of canine heart endothelial nitric oxide synthase cDNA and 5'-flanking sequence by homology (RT-)PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Ćhordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
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                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-LUNG;
Bachmann S., Bostanjoglo M., Nafz B., Oberbaeumer I.;
No synthases in the kidney.";
Submitted (SPE-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ249546; CAB77547.1;
InterPro; IPR001709;
InterPro; IPR003099;
FALDLAMP PRO0667; FAD_Dinding; 1.
PRINTS; PR00671; FAD_Dinding; 1.
                                                                                                                                                                                                                                                                                        Obstratement I., Welp H., Bachmann S.;
"A cDNA probe for rat NOS3 for in situ hybridization.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 AA; 33803 MW; 6466628BF253EE13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
NITRIC OXIDE SYNTHASE.
                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ENDOTHELAL NITRIC OXIDE SYNTHASE 3 (FRAGMENT).
306 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1205 AA
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EMBL; AF143503; AAD52161.1; -.
HSSP; P29474; 3NOS.
InterPro; IPR001094; -.
InterPro; IPR001433; -.
InterPro; IPR001409; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GIVPFRSFWQQRLHD 15
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Sphingiodea; Sphingidae; Sphinginae; Manduca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDIAGE-9736646; MIDDED A. GIBSON N.J. Rivers D.M., Hildebrand J.G., Morton D.B.; Wighborn A., Gibson N.J., Rivers D.M., Hildebrand J.G., Morton D.B.; "The nitric oxide-cGMP pathway may mediate communication between sensory afferents and projection neurons in the antennal lobe of
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Pred. No. 0.54;
                                                                                                                                                       Length 1205;
                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
                                                                                               C150CDEB01685BA5 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
NITRIC-OXIDE SYNTHASE (EC 1.14.13.39) (DNOS).
                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                       Score 71; DB 6;
Pred. No. 0.0016;
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                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                               1205 AA; 133045 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Neurosci. 18:7244-7255(1998).
EMBL; AF062749; AAC61262.1; -
HSSP; P29477; 1DD7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1206 AA; 137032 MW;
InterPro; IPR003097; -.
Pfam; PF00175; oxidored_fad; 1.
Pfam; PF00667; PAD_binding; 1.
PRIWTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR00369; FLAVODOXIN.
                                                                                                                                                         68.9%;
80.0%;
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Best Local Similarity 44.47
Best Local 8; Conservative
                                                                                                                                                       Query Match 68.9
Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                                                                                  1 GIVPFRSFWQQRLHD 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001094; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001433; -. InterPro; IPR003097; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NITRIC OXIDE SYNTHASE.
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                                                                                                 SEQUENCE
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11D D77104
11D D77109
10D D77104
10D
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RESPONDER FROM N. A.

READURE S. C. Scherer S. E. LID PW. Hostkins R. A. Galls R. P.

R. GOOTGE R. A. Leavis S. E. Kicharids S. Abburner W. Henderson S. N.,

SHICHOUGH C. C. Mortman J. R. Yandell H. D. Jahang Q. Chen L. X.

READURE FROM N. A.

READURE FROM N. FOR P. Y. Berman B. P. Bhandarl D. Bollahkov S.

R. Berndon R. C. Boyler P. Y. Berman B. P. Bhandarl D. Bollahkov S.

R. Berndon R. C. Mosers Y. Hender R. C. Change R. Felling I.

READURE FROM D. BOCKCHAN H. R. BORK J. J. Berndon B. P. Berndon R. C. Change R.

R. Berldon R. C. Boyler D. L. Bollahkov S. M.

R. Berndon R. C. Wolley S. Deller T. A. Deng Z. Mays A.D. Devil. Dollar E. S. M.

R. Berndon R. C. Mosers D. A. Buller H. Caddau E. Conter A. Change I. Deller T. A. Deng Z. Mays A.D. Devil. Dollar E. S. M.

R. Berndon R. C. Mosers D. M. Berndon B. P. Bhandarl D. Bollar B. M. G.

R. Bortova D. Bockler T. A. Deng Z. Mays A.D. Devil. Dollar E. S. M.

R. Berndon R. C. Gootel M. R. M. Mork J. W. Bork J. M. Bortova D. Bockler T. A. Deng Z. Mays A.D. Devil. Dollar E. S. M.

R. Berndon R. C. Gootel J. E. Sander R. F. Combart W. M. J. Book J. J.

R. Marcia B. M. More P. G. Gortall J. H. G. Z. Mennison J. M. Metzon B. J. M.

R. Mostin D. M. Houston R. A. Wolland T. J. Herninge Z. Mays A.D. May R. Mellen B. M. Mouth S. M. Mouth S. M. Moor M. M. Mozon R. M. Mo
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320 AA

PRELIMINARY;

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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
FERREDOXIN-NADP REDUCTASE (EC 1.18.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: September 10, 2001, 14:11:11
Job time: 590 sec
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ID Q9S9E0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=137C;
MEDLINE=55142635; PubMed=7840625;
Decottignies P., Le Marechal P., Jacquot J.P., Schmitter J.M.,
Gadal P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
FERREDOXIN NADP REDUCTASE (EC 1.18.1.2) (FERREDOXIN--NADP(+)
                                                                                                                                                                                                                                                                                                                                                     54.4%; Score 56; DB 5; Length 1349;
81.8%; Pred. No. 0.6;
Live 1; Mismatches 1; Indels
                                                        Incerto; irrussos,;

Pfam; PF0015; oxidored_fad; 1.

Pfam; PF0015; EAD-binding; 1.

PRINTS; PR00369; FLAVODOXIN.

PRINTS; PR00311; FPNCR.

PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.

Oxidoreductase; NAPP; FAD; FMN; Calmodulin-binding; Heme;
Alternative splicing.

CONFLICT 373 373 T -> S (IN REF. 2).
                                                                                                                                                                                                                                     373 373 T -> S (IN REF. 2).
1197 1197 S -> R (IN REF. 2).
1349 AA; 151713 MW; E19DBCBAEFAF76FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       628CFED2592A1999 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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InterPro; IPR001709; -.
Pfam; PF00175; oxidored_fad; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255
28594 MW;
                                                                                                                                                                                                                                                                                                                                                       Query Match 54.4
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
InterPro; IPR001709; -. InterPro; IPR001993; -. InterPro; IPR003097; -.
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255 AA;
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NON_TER
SEQUENCE
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042697
0D 701-NOV-
DT 01-NOV-
DT 01-NOV-
DT 01-NOV-
DE FERREDO
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CO COLLAMY-
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CONTENT-
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Gaps

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1; Indels

Query Match 49.5 Best Local Similarity 72.7 Matches 8; Conservative

|| ||||||:: 115 GIAPFRSFWRR 125

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15

RESULT

1 GIVPFRSFWQQ 11

Length 255;

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"Primary structure and post-translational modification of ferredoxin-NADP reductase from Chlamydomonas reinhardtii.";
Arch. Biochem. Biophys. 316:249-259(1995).
HSSP; P00455; IFNC.
InterPro; IPR001433; -.
InterPro; IPR001709; -.
Pfam; PF00175; oxidored_fad; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Chlamydomonas reinhardtii.
Vakaryota, Virldiplantee; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                MEDLINE-95142635; PubMed-7840625;
Decottignies P., Le Marechal P., Jacquot J.P., Schmitter J.M.,
Gadal P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 10; Length 320;
Pred. No. 0.95;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        320 AA; 35571 MW; DB7897520C5B87E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00371; FPNCR
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180 GIAPFRSFWRR 190
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 10, 2001, 14:00:31 ö Run

; Search time 23.82 Seconds (without alignments) 25.886 Million cell updates/sec

1 GIVPFRSFWQQRLHDSQH 18 US-08-833-506C-25 103 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

93435 seqs, 34255486 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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	ption	oryctolagus	mus musculu	rattus norv	homod	homo	homo	cavia		mus musculu	rattus norv	homo sa	gallus gall	homo sa	_	sus scrofa	rattus norv	mus musculu	lymnaea sta	_		-	-		_		chlamydomon	candida gla	catharanthu	rattus norv	homo sapien	schizosacch		thiocapsa r
	Description	019114	P29477	006518	P35228	060591	014961	054705	027995	0920j4	P29476	P29475	090703	P29474	P29473	028969	062600	P70313	061309	019132	026240	061608	027571	P57503	P38038	P38039	P53991	P50860	00200	P31421	P81272	009744	010325	P52674
	ID	NOS2_RABIT	NOS2_MOUSE	NOS2_RAT	NS2A_HUMAN	NS2D_HUMAN	NS2C_HUMAN	NOS2_CAVPO	NOS2_BOVIN	NOS1_MOUSE	NOS1_RAT	NOS1_HUMAN	NOS2_CHICK	NOS3_HUMAN	NOS3_BOVIN	NOS3_PIG	NOS3_RAT	NOS3_MOUSE	NOS_LYMST	NOS1_RABIT	NOS_RHOPR	NOS_ANOST	NOS_DROME	CYSJ_BUCAI	CYSJ_ECOLI	CYSJ_SALTY	FENR_CHLRE	ERG3_CANGA	NCPR_CATRO	MGR2_RAT	NS2B_HUMAN		хрбр_ѕснро	CYSJ_THIRO
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٠	Match Length DB	496	1144	1147	1153	1147	69	1149	246	1429	1429	1434	1136	1202	1204	1204	919	1201	1153	1435	1174	1247	1350	601	298	598	354	364	714	872	79	571	407	522
s Ouerv	Match	96.1	96.1	96.1	96.1	88.3	83.5	81.6	76.7	75.7	75.7	75.7	73.8	72.8	72.8	72.8	70.9	70.9	67.0	0.99	57.3	55.3	54.4	51.5	50.5	50.5	49.5	45.6	44.7	44.7	43.7	43.7	42.7	42.7
	Score	66	66	66	66	91	98	84	79	78	78	78	92	75	75	75	73	73	69	68	29	57	26	53	52	52	51	47	46	46	45	45	44	44
Result	No.	1	7	3	4	S	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33

P18834 caenorhabdi P45745 bacillus su P00454 spirulina s P31973 synechococc Q55318 synechococc Q55318 synechocyst P31477 euglena gra Q44763 borrelia bu P51606 homo saplen P51607 rattus norv Q60759 mus musculu Q28125 bos taurus P25351 saccharomyc
CC14_CAEEL DHBF_BACSU ENRR_SPISP FENR_SYNP2 FENR_SYNY3 AIPE EUGGR FLIP_BORBU RNBP_RAT GCDH_MOUSE ICA3_YEAST
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ALIGNMENTS

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                                                                                                                                                                                                FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC OXIDE SYMTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
(INDUCIBLE NOS) (INOS) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NADP; FAD; FMN; Calmodulin-binding; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EWN (PYRIMIDINE PART) (BY SI
149 FAD (ADP PART) (BY SIMILARIT
284 FAD (FLAVIN PART) (BY SIMILA
367 NADP (RIBOSE PART) (BY SIMILA
462 NADP (ADP PART) (BY SIMILARI
496 NADP (ADP PART) (BY SIMILARI
               496 AA
                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: HÖMÖDIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NOS FAMILY.
               PRT;
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Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U85094; AAB65618.1; -. HSSP; P00388; 1AMO.
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001433; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274
349
447
496
496 AA;
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Multigene family.

NON_TER 1

NP_BIND 138

NP_BIND 274

NP_BIND 274

NP_BIND 447

NON_TER 496

SEQUENCE 496 AA;
                                                                                                                                                                         NCBI_TaxID=9986;
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               NOS2_RABIT
                            019114;
NOS2_RABIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-92357701; Pubmed-1379716;
LOWenstein C.J., Glatt C.S., Bredt D.S., Snyder S.H.;
LOwenstein G.Y., Glatt C.S., Bredt D.S., Snyder S.H.;
Loned and expressed macrophage nitric oxide synthase contrasts with
the brain enzyme.";
Proc. Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
MEDLINE-20031637; Pubmed-10562538;
Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhui R., Crooks C.,
Presta A., Tainer J.A., Getzoff E.D., Stuchr D.J.;
"Inducible nitric oxide synthase: role of the N-terminal beta-hairpin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN DBA/2J, BALB/CBYJ, SJL/J, NOD/LTJ, AND B10.S/J; TISSUE Spleen; Ma R.Z., Teuscher C.; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-92210618; PubMed-1372907;
Lyons C.R., Orloff G.J., Cunningham J.M.;
Molecular cloning and functional expression of an inducible nitric oxide synthase from a murine macrophage cell line.";
J. Biol. Chem. 267:6370-6374(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E.D.
                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Sukaryota i Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96088781; PubMed-7503239; Kone B.C., Schwoebel J., Turner P., Mohaupt M.G., Cangro C.B.; Role Go NF-kappa B in the regulation of inducible nitric oxide synthase in a MTAL cell line "; Am. J. Physiol. 269:F718-F729(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 116-496.
MEDLLIBE-97477482; PubMed-9334294;
MEDLLIBE-97477482; PubMed-9334294;
Crane B.R., Arvai A.S., Gachhui R., Wu C., Ghosh D.K., Getzoff Stuehr D.J., Tainer J.A.;
"The structure of nitric oxide synthase oxygenase domain and inhibitor complexes.";
Science 278:425-431(1997).
                                        .;
0
                                                                                                                                                                                                 NOSZ_MOUSE STANDARD; PRT; 1144 AA.
P29477; O70515; O70516;
01-APR-1993 (Rel. 25, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
NITRIC OXIDE SYNTHASE, INDUCIBLE (RC 1.14.13.39) (NOS, TYPE (INDUCIBLE NOS) (MACROPHAGE NOS) (MAC-NOS).
Score 99; DB 1; Length 496;
Pred. No. 3.6e-09;
0; Mismatches 1; Indels
 96.1%;
94.4%;
                                                                                                356 GIAPFRSFWQQRLHDSQH 373
                                                                         1 GIVPFRSFWQQRLHDSQH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse macrophages.";
Science 256:225-228(1992).
                 Local Similarity 94.4 ies 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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 Query Match
                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN HINBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CAPALYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE
                                                                                                                                                                                                                                                                                                                                                                TISSUE-Macrophage;
MEDLINE=95372392; PubMed=7544010;
MEDLINE=95372392; PubMed=7544010;
Amin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,
Welssmann G., Abramson S.B.;
"The mode G, Abramson S.B.;
"The mode of action of aspirin-like drugs: effect on inducible nitric oxide synthase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).

-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO MEDIAPES TUMORICIDAL AND BACTERICIDAL ACTIONS.

-!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE + NITRIC OXIDE + N NADP(+).

-!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.
MEDLINE-98182450; PubMed-9516116;
Crane B.R., Arvai A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,
                                                                                                                                  "Structure of nitric oxide synthase oxygenase dimer with pterin and substrate ".
                                                                                                                                                                                                                           MEDLINE-20031638; PubMed-10562539; "Carne B.K., Rosenfeld R.J., Arval A.S., Ghosh D.K., Ghosh S., Tainer J.A., Stuchr D.J., Getzoff E.D.," Neterminal domain swapping and metal ion binding in nitric oxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: HOMODIMER.
-!- TISSUE SPECIFICITY: MACROPHAGES.
-!- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES.
-!- SIMILARITY: BELONGS TO THE NOS FAMILY.
 in dimerization and
                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF065922; AAC17917.1; ALT_INIT. AF065923; AAC17918.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M92649; -; NOT_ANNOTATED_CDS.
EMBL; M84373; AAA39834.1; -.
EMBL; U43428; AAC52356.1; -.
hook and pterin-binding segment itetrahydrobiopterin interaction. EMBO J. 18:6260-6270(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF065919; AAC17914.1; -. AF065920; AAC17915.1; -. AF065921; AAC17916.2; -.
                                                                                                                                                                         Science 279:2121-2126(1998).
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18-NOV-98.
23-MAR-99.
23-MAR-99.
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08-DEC-99.
04-FEB-00.
06-FEB-00.
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A42166; A42166
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                                                                                                                           Tainer J.A.;
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SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                               FMN (PYRIMIDINE PART) (BY SIMÍLARITY).
FAD (ADP PART) (BY SIMÍLARITY).
FAD (FLAVIN PART) (BY SIMÍLARITY).
NADP (RIBOSE PART) (BY SIMÍLARITY).
NADP (ADP PART) (BY SIMÍLARITY).
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Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,
Mandrup-Poullsen T., Boel E., Nerup J.;
"Cloning and expression of cytokine-inducible nitric oxide synthase
cDNA from rat islets of Langerhans.";
Diabetes 44:753-758(1995).
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TISSUE-Vascular smooth muscle;
MEDLINE-93191721; Pubmed-7680561;
Nunokawa Y., Ishida N., Tanaka S.;
"Cloning of inducible nitric oxide synthase in rat vascular smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OG6518; P97774; O35765; O35766; O64558; Q64005; Q63267; O1-JUN-1994 (Rel. 29, Created) O1-OCT-1996 (Rel. 34, Last sequence update) O1-OCT-2000 (Rel. 34, Last sequence update) NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II) NITRIC OXIDE NOS) (INOS).
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-> F (IN STRAIN BALB/CBYJ).

-> T (IN REF. 4).

-> V (IN REF. 2).

0735BE676113457F CRC64;
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                                                                                                                                                                                                                                                                                                             Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> R (IN STRAIN NOD/LTJ).
-> L (IN STRAIN SJL/J).
-> F (IN STRAIN BALB/CBYJ
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STRAIN-WISTAR; TISSUE-Pancreatic islets;
MEDLINE-95309542; PubMed-7540573;
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Pfam; PF00175; oxidored_fad; 1.
PRIWTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
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94.4%;
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Best Local Similarity 94.4'
Matches 17; Conservative
                                                                   MGD; MGI:97361; NOS2.
InterPro; IPR001094; -.
InterPro; IPR001433; -.
InterPro; IPR001709; -.
InterPro; IPR003097; -.
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1DWX;
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SEQUENCE OF 426-788 FROM N.A.
STRAIN-DAHL/RAPP SALT SENSITIVE STRAIN; TISSUE-Vascular smooth muscle;
MEDLINE-98195092; PubMed-9535415;
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MEDLINE=93221515; PubMed=7682072;
Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
"Hepatocytes and macrophages express an identical cytokine inducible nitric oxide synthase gene.";
Biochem. Biophys. Res. Commun. 191:767-774(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=SPRAGUE-DAWLEY, TISSUE-Aorta;
MEDLINE=94325351; PubMed=7519448;
Geng Y.J., Almquist M., Hansson G.K.;
"CDNs cloning and expression of inducible nitric oxide synthase from rat vascular smooth muscle cells.";
Biochim. Biophys. Acta 1218:421-424(1994).
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"Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Futaki S., Niwa M.;
"Sequence analysis of inducible nitric oxide synthase in rat kidney,
lung, and uterus." 19:1374-1376(1996).
Biol. Pharm. Bull. 19:1374-1376(1996).
                                                                                                             nitric oxide synthase from rat
                                                                                                                                                                                                                                                                                                                                                    Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K., Kawasaki H., Sugimura T., Esumi H.; Molecular cloning of a cDNA encoding an inducible calmodulin-dependent nitric-oxide synthase from rat liver and its expression in COS I cells.";
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Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S
"Advances in the studies of NO synthesis regulation in mesanglial
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Kosuga K., Yui Y., Hattori R., Sase K., Eizawa H., Aoyama T.,
Inoue R., Sasayama S.;
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Tsutsumishita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning of an inducible nitric oxide synthase from rat
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STRAIN-SPRAGUE-DAWLEY; TISSUE-Astrocytes; BDDLINE-94211594; PUDMed-7513765; Galea E., Reis D.J., Feinstein D.L.; "Cloning and expression of inducible nitr
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                              Neurosci. Res. 37:406-414(1994).
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Endothelium 2:217-221(1994).
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                                                                                                                                                                                                                                                                                                                              MEDLINE=94039059; PubMed=7693462
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Hypertension 31:918-924(1998).
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Kidney Int. 45:998-1005(1994).
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                                                                                                                                                                                                                       SUBUNIT: HÖMODIMER (BY SIMILARITY).
TISSUE SPECIFICITY: IN NORMAL KIDNEY, EXPRESSED PRIMARILY IN THE
MEDULLARY THICK ASCENDING LIMB, WITH MINOR AMOUNTS IN THE
MEDULLARY COLLECTING DUCT AND VASA RECTA BUNDLE.
INDUCTION: BY INTERFERON GAMMA AND LIPOPOLYSACCHARIDE.
SIMILARITY: BELONGS TO THE NOS FAMILY.
     THE ENZYME.
ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN
ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN
INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE
EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL
MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY
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HEME (BY SIMILARITY).

CALMODULIN-BINDING (POTENTIAL).

FAND (ADP PART) (BY SIMILARITY).

FAD (ADP PART) (BY SIMILARITY).

FAD (RIBOSE PART) (BY SIMILARITY).

NADP (RIBOSE PART) (BY SIMILARITY).

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ZINC (BY SIMILARITY).
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InterPro: IPR001433; ...
InterPro: IPR001433; ...
InterPro: IPR001709; ...
Pfam; PF00067; FAD_binding; 1...
Pfam; PF00175; oxtdored_fad; 1...
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
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BINDING 197 197 HE
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MEDLINE-94032282; PubWed=7622964;
MEDLINE-94032282; PubWed=7622964;
Sherman P.A., Laubach V.E., Reep B.R., Wood E.R.;
Purification and cDNA sequence of an inducible nitric oxide synthase from a human tumor cell line.";
Biochemistry 32:11600-11605(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver;
MEDLINE-9334523; PubMed-7682706;
MEDLINE-9334523; PubMed-7682706;
Geller D.A., Lowenstein C.J., Shapiro R.A., Nussler A.K.,
di Silvio M., Wang S.C., Nakayama D.K., Simmons R.L., Snyder S.H.,
Billiar T.R.;
"Molecular coloning and expression of inducible nitric oxide synthase
from human hepatocytes."
Proc. Natl. Acad. Sci. U.S.A. 90:3491-3495(1993).
                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Chondrocytes;
MEDLINE=94068614; PubMed=7504305;
Charles I.G., Palmer R.M.J., Hickery M.S., Bayliss M.T.,
Chubb A.P., Hall V.S., Moss D.W., Moncada S.;
Cloning, characterization, and expression of a cDNA encoding an
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P3522B; 016092; 060757; 016263;
01-FEB-1994 (Rel. 28, caeted)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC OXIDES SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE INDUCIBLE NOS) (INDS) (HEPATOCYTE NOS) (HEP-NOS).
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                                                             POZSKRKRUDO
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96.18;
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583
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J. В
[13]
  "Continuous nitric oxide synthesis by inducible nitric oxide synthase in normal human airway epithelium in vivo."; Proc. Natl. Acad. Sci. U.S.A. 92:7809-7813(1995).
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                                              TISSUE-Articular chondrocytes;
MEDLINE=94368816; PubMed=7522054;
MAider R., Bilbe G., Rediske J., LOLZ M.;
Inducible nitric oxide synthase from human articular chondrocytes:
cDNA cloning and analysis of mRNA expression.";
Biochim. Biophys. Acta 1208:145-150(1994).
                                                                                                                                                                   Park C.S., Pardhasaradhi K., Gianotti C., Villegas B., Krishna G.; "Human retina expresses both constitutive and inducible isoforms of nitric oxide synthase mRNA.";
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MEDLINE-95155267; PubMed-7531687;
Hokari A., Zeniya M., Esumi H.;
"Cloning and functional expression of human inducible nitric oxide synthase (NOS) cDNA from a glioblastoma cell line A-172.";
J. Biochem. 116:575-581(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96047340; PubMed-7558036; Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G., Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.; "Three members of the nitric oxide synthase II gene family (NOS2A, NOS2B, and NOS2C) colocalize to human chromosome 17."; Genomics 27:526-530(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McLay J.S., Chatterjee P., Nicolson A.G., Jardine A.G., McKay N.G. Ralston S.H., Grabowski P., Haites N.E., Macleod A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Cardiac myocytes;

BEDLINE-2704504, PubMed-9160867;
Luss H., Li R.-K., Shapiro R.A., Tzeng E., McGowan F.X., Yoneyama Hatakayama K., Geller D.A., Mickle D.A.G., Simmons R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Billiar T.R.; Dedifferentiated human ventricular cardiac myocytes express inducible nitric oxide synthase mRNA but not protein in response IL-1, TNF, IFNgamma, and LPS.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MEDLINE-98389865; PubMed-9721329;
Taylor B.S., Alarcon L.H., Billiar T.R.;
"Inducible nitric oxide synthase in the liver: regulation and
inducible nitric oxide synthase from the human chondrocyte."; Proc. Natl. Acad. Sci. U.S.A. 90:11419-11423(1993).
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X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 74-504
                                                                                                                                                                                                         iochem. Biophys. Res. Commun. 205:85-91(1994).
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                                                                                                                                              TISSUE=Retina;
MEDLINE=95091827; PubMed=7528017;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Airway epithelium;
MEDLINE-95372368; PubMed-7544004;
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MEDLINE-95165725; PubMed-7532248;
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Xidney Int. 46:1043-1049(1994).
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CONTINUE FUNCTIONS THROUGHOUT THE BODY. IN MACROHAGES, NO
MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.

COTALLY CATALLY ACTURY: LARGININE + N NADPH + M O(2) = CITRULLINE +
NITRIC OXIDE + N NADP(+).

COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FWN. ALSO REQUIRES
TETRAHYDROBOPOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
THE BNZYME (BY SIMILARITY).

COFACTOR: REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST
THE ENZYME (BY SIMILARITY).

COFACTOR: REGULATION REGULATION AND FUNCTION OF THIS
ENZYME AND PEFFECTS MAY BE EXERTED AT THE LEVEL OF
TRANSLATIONAL/POSTTRANSLATIONAL WODIFICATION AND DIRECTLY ON THE
COTALLYTIC ACTIVITY (BY SIMILARITY).

COFACTOR SPECIFICITY: EXPRESSED IN THE LIVER, RETINA, BONE CELLS AND
ARRAY EPITHELIAL CELLS OF THE LUNG. NOT EXPRESSED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reveals striking active-site conservation.";
Nat. Struct. Biol. 6:233-242(1999).
-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
                             Li H., Raman C.S., Glaser C.B., Blasko E., Young T.A., Parkinson J.F., Whitlow M., Poulos T.L.;
"Crystal structures of zinc-free and -bound heme domain of human inducible nitric-oxide synthase. Implications for dimer stability and comparison with endothelial nitric-oxide synthase.";
J. Biol. Chem. 274:21276-21284(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CALMODULIN-BINDING (POTENTIAL).
FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 82-528.
MEDLINE=99173237; PubMed=10074942;
Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,
Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,
Weber P.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Structural characterization of nitric oxide synthase isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: BELONGS TO THE NOS FAMILY.
MEDLINE-99340067; PubMed-10409685;
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EMBL, L24553; AAA51512.1; -
EMBL, X73029; CAA51512.1; -
EMBL, U05810; AAA5666.1; -
EMBL, U31511; AAA49041.1; -
EMBL, D26525; BAA05531.1; -
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EMBL; S75615; AAD14179.1; --
PIR; A47475; A47475.
PDB; 1NSI: 07-JAN-00.
PDB; 2NSI: 07-JAN-00.
PDB; 4NOS; 04-FEB-00.
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PRINTS; PR00371; FPNCR.
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send an email to license@isb-sib.ch)
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MEDLINE-96047340; PubMed-7558036;
                                                                                          InterPro; IPR003097; -.
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
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94.1%;
                       EMBL; AF049656; AAC83553.1;
EMBL; AF051164; AAC83554.1;
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                                                                    InterPro; IPR001433; -. InterPro; IPR001709; -.
                                                          InterPro; IPR001094;
                                                                                                                                                                  Heme; Zinc; Metal-bi
BINDING 197 1
                                              HSSP; P29477; INOC
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Matches 16; Conserv
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014961;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO MEDIATES FUNCATIONS THROUGHOUS. MY BE INVOLVED IN THE PATHGENESIS OF DILATED CARDIOMYOPATHY OR OF EXERCISE INTOLERANCE OBSERVED IN PATIENTS WITH CHRONIC HEART FAILURE.

CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE + OFFICE OXIDE + N NADP(+).

COFACTOR: HEMB: BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TERMYDROBOPTERIN (BH4) WHICH MAX STABILIZE THE DIMERIC FORM OF
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06051; 060604;
30-MAY-2000 (Rel. 39, Last sequence update)
310-MAY-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
NITRIC OXIDE SYNTHASE, INDUCIBLE IID (EC 1.14.13.39) (NOS, TYPE II (INDUCIBLE NOS) (INOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HÖMODIMER (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED IN THE HEART AND SKELETAL MUSCLE
DURING CHRONIC HEART FAILURE, BUT NOT IN HEALTHY INDIVIDUALS.
SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                             (POTENTIAL)
                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Skeletal muscle, and Heart muscle;
MEDLINE-9906690; PubMed-9851365;
Adams V., Krabbes S., Jiang H., Yu J., Rahmel A., Gielen S.,
Schuler G., Hambrecht R.;
"Complete coding sequence of inducible nitric oxide synthase from human heart and skeletal muscle of patients with chronic heart
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            (RIBOSE PARÍ) (BY SIMILARITÝ).
(ADP PARÍ) (BY SIMILARITÝ).
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 (FLAVIN PART) (BY SIMILARITY)
                                                                                                                                                                                                             Length 1153;
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ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (BY
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                                                          CAPK)
CAPK)
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(IN REF. 4).
(IN REF. 9).
(IN REF. 2).
(IN REF. 5).
(IN REF. 5 AND 6).
(IN REF. 7).
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                                                           PHOSPHORYLATION
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0; Mismatches
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Nitric Oxide 2:242-249(1998)
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154
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423
439
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800
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996
1091
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115
234
578
892
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
                                                                                                                                                                                                                                   17;
                                                                                                                            CONFLICT
CONFLICT
CONFLICT
                                                                                                      CONFLICT
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                                                                                                                                                                                                             Query Match
           NP_BIND
NP_BIND
METAL
METAL
                                                         MOD_RES
MOD_RES
MOD_RES
                                                                                            CONFLICT
                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                    RESULT 5
NS2D_HUMAN
                                                                                                                                                                                                                                      Matches
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-I- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +
                                                        HEME (BY SIMILARITY).

CALMODULIN-BINDING (POTENTIAL).

FAM (PYRIMIDINE PRART) (BY SIMILARITY).

FAD (ALAP PART) (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).

ZINC (BY SIMILARITY).

ZINC (BY SIMILARITY).

ZINC (BY SIMILARITY).

ZINC (BY SIMILARITY).

A - S (IN AAC83554).

C -> E (IN AAC83554).

A -> T (IN AAC83554).

A -> T (IN AAC83554).

A -> T (IN AAC83554).

C -> E (IN AAC83554).

A -> T (IN AAC83554).

C -> E (IN AAC83554).

C -> E (IN AAC83554).

C -> E (IN AAC83554).

C -> I (IN AAC83554).

TL -> NF (IN AAC83554).

TL -> NF (IN AAC83554).

T -> NF (IN AAC83554).
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Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;
Heme; Zinc; Metal-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC-OXIDE SYNTHASE IIC (EC 1.14.13.39) (NOS, TYPE II C) (NOSIIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G., Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.; Three members of the nitric oxide synthase II gene family (NOS2A, NOS2B, and NOS2C) colocalize to human chromosome 17."; Genomics 27:526-530(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FF7E4C7ABA76D820 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 91; DB 1;
Pred. No. 2e-07;
0; Mismatches
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Best Local Similarity
Matches 14; Conserv
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622
766
902
977
                                                                                                                                                                                                                                                                                                                         HSSP; P29477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               macrophages.
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NP_BIND
SEQUENCE
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NP_BIND
NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
NOS2_BOVIN
     g
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                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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STRAIN-HARTLEY; TISSUE-Lung;
MEDLINE-98343971; PubMed-9677342;
MIDLINE-98343971; PubMed-9677342;
Shirato M., Sakamoto T., Uchida Y., Nomura A., Ishii Y., Iijima H.,
Goto Y., Hasegawa S.;
"Molecular cloning and characterization of Ca2+-dependent inducible
nitric oxide synthase from quinea-pig lung.";
Blochem. J. 333:795-799(1998).
-I- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
WITH DIVERSE FUNCTIONS THROUGHOUT THE BODD.
NITRIC OXIDE + N NADP(+).
COPACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE + N NTRIC OXIDE + N NADP(+).
-!- COFACTOR: HEME. BINDS OWE MOLE EACH OF FAD AND FWN. ALSO REQUIRES TETRAHYDROBIOPPERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMODIMER (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED IN THE LUNG AND COLON. NOT DETECTED IN THE HEART, AORTA, LIVER, KIDNEY, AND SPLEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;
Heme; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE ENZYME (BY SIMILARITY).
ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADP (RIBOSE PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
NITRIC OXIDE SYMTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                       THE ENZYME (BY SIMILARITY).
ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86; DB 1; Leuy...
Pred. No. 6.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2C29D595F93FB293 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                              SUBUNIT: HOMODIMER (BY SIMILARITY). SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U18335; AAC50245.1; -. EMBL; U18334; AAC50245.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8432 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 83.5
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WITH MOUSE NOS2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                       SIMILARITY)
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054705;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding; Heme; Multigene family.

BINDING 199 199 HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CALMODULIN BINDING (POTENTIAL).
FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
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MEDLINE-96047340; PubMed-7558036;
Bloch K.D., Wolfram J.E., Brown D.M., Roberts J.D. Jr., Zapol D.G.,
Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
-!- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS) IN KIDNEY, SPLEEN, AN COLON. EXPRESSION IS REDUCED IN THE PRESENCE OF LPS IN LUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOS2_BOVIN STANDARD; PRT; 246 AA. 027952; 027985; 027985; 027985; 02.01-00V-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) A30-MAY-2000 (Rel. 39, Last annotation update) NITRC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II) (INDUCIBLE NOS) (INOS) (NOSII) (FRAGMENTS).
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Pred. No. 3e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
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                                                                                                                                                                                                                                                                                                                                InterPro; IPR001094; --
InterPro; IPR001433; --
InterPro; IPR001709; --
InterPro; IPR003097; --
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
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                                                                                                                                                                                                                                                                                        EMBL; AF027180; AAC33177.1; -.
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00369; FLAVODOXIN PRINTS; PR00371; FPNCR.
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NCBL_TaxID=9913;
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MEDLINE-96212184; PubMed-862668;
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                                                                                                                                                                                                                                                                               I- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS ACTIONS I- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) · CITRULLINE +
                                                                                   NITRIC OXIDE + N NADP(+).

COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF THE ENZYME (BY SIMILARIY).

ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ogura T., Yokoyama T., Fujisawa H., Kurashima Y., Esumi H.; "Structural diversity of neuronal oxide synthase mRNA in the nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE I) (NEURONAL
"Three members of the nitric oxide synthase II gene family (NOS2A, NOS2B, and NOS2C) colocalize to human chromosome 17."; Genomics 27:526-530(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó;
                                                                                                                                                                                                                                                                                                                                                                                      HEME (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 79; DB 1; Length 246;
Pred. No. 3.8e-06;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       Pfam; PF00175; oxidored_fad; 1.
Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOSI_MOUSE STANDARD; PRT; 1429 AA. 0920J4; 064208; 30-MAY-2000 (Rel. 39, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS).
                                                                                                                                                                                                                                                                                                                                                                                                                         246
28748 MW; 87C2E330C86A27F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 193:1014-1022(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS N-NOS-1 AND N-NOS-2)
                                                                                                                                                         SUBUNIT: HÖMODIMER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM NNOS MU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB/C; TISSUE-Brain;
MEDLINE-93312283; PubMed-7686743;
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e
                                                                                                                                                                                                                                                                                         EMBL; U14640; AAC48470.1; -. EMBL; U18331; AAC48479.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.7%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 PFRSFWQQRLHEAEH 126
                                                                                                                                                                                                                                                                                                                              ; IPR001433; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 PFRSFWQQRLHDSQH 18
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215
111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                  3NOD
                                                                                                                                                                                                                                                                                                                                                              Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                                 HSSP; P29477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
NON_CONS
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                              InterPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
NOS1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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THE DYSTROPHINTER. ISOFORM NNOS MU MAY BE AN BEFECTOR ENZYME FOR THE DYSTROPHIN COMPLEX.

1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE + NITRE OXIDE + N NADP(+).

1- NITRE OXIDE + N NADP(+).

1- COFACTOR: HERE. BINDS OWE MOLE EACH OF FAD AND FMN. ALSO REQUIRES THE ENZYME REGULATOR: STIMULARITY).

1- SUBCHILLATE BENEVER REGULATION: STIMULARITY).

1- SUBCHILLATE ROCATION: STIMULARITY).

1- SUBCHILLATE LOCATION: IN SKELETAL MUSCLE, NNOS IS LOCALIZED BENEVERT THE DIMERIZATION OF THE PROTEIN (BY SIMILARITY).

1- SUBCHILLATER LOCATION: IN SKELETAL MUSCLE, NNOS IS LOCALIZED BENEVERT THE DYSTROPHIN GLYCOPOTEIN COMPLEX.

1- SUBCHILLATER LOCATION: IN SKELETAL MUSCLE-SPECIFIC; ARE PRODUCED ALSO FOUND THE SALTERNATIVE SPILICING.

2. NNOS BETA, NNOS GAMAA AND NNOS MU/MUSCLE-SPECIFIC; ARE PRODUCED STERBELLING. PONS, MEDULLA ORDINGATA, AND SPIRAL COMPLEX.

2. NNOS BETA, NNOS GAMAA AND NNOS MU/MUSCLE-SPECIFIC; ARE PRODUCED IN SKELETAL MUSCLE, WHERE IT IS LOCALIZED BENEATH THE SACCOLEMAA OF FAST THICH MUSCLE FIBERS, AND IN SPLEEN HEART, KIDNEY, AND LIVER. NNOS BETA AND GAMAA OCCUR IN A REGION-SPECIFIC MANNER IN THE BRAIN AND NNOS BETA AND GAMAA OCCUR IN A REGION-SPECIFIC MANNER IN THE BRAIN AND NNOS BETA AND GAMAA OCCUR IN A REGION-SPECIFIC MANNER IN THE BRAIN AND NNOS BETA EXPRESSION IN ALIE BRAIN AND NNOS BETA EXPRESSION IN AND IN SELECTAL AND CANDITAE SKELETAL AND CANDITAE THE BRAIN AND NNOS BETA EXPRESSION IN AND IS SKELETAL BRAIN AND NNOS BETA EXPRESSION IN THE PAR OF THE BRAIN AND SETAL ENGY OF THE BRAIN AND SETAL ENGY OF THE NOS TO SYNAPTIC MUSRARALLY THE DECREPORE.

1- INDUCTION: THE PDZ DOMAIN IN THE NETRACTION, AND IS SEADONISHED FOR THE NOS TO SYNAPTIC MUSRARALLY THE DECREPORE. IN THE WILLY SHAPPOLY.

2- SERBENDALING COMPLEX IS DISRUPTED AND NNOS IS DISPLACED FROM SARROLLEMAN AND ACCOUNTARTS IN THE CYTOSOL.

2- SIMILARITY: BELONGS TO THE NOS FAMILY.

2- SIMILARITY: BELONGS TO THE NOS FAMILY.

3- SHALLARITY: BELONGS TO THE NOS FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. Neurosci. 19:224-231(1997).

-i- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN THE BRAIN AND PERIPHERAL NERVOUS SYSTEM, NO DISPLAYS MANY PROPERTIES OF A NEUROTRANSMITTER. ISOFORM NNOS MU MAY BE AN EFFECTOR ENZYME FOR
Silvagno F., Xia H., Bredt D.S.;
"Neuronal nitric-oxide synthase-mu, an alternatively spliced isoform expressed in differentiated skeletal muscle.";
J. Biol. Chem. 271:11204-11208(1996).
                                                                                                                                                                                                                                                                                                MEDLINE-97351924; PubMed-9208206;
Brenman J.E., Xia H., Chao D.S., Black S.M., Bredt D.S.;
"Regulation of neuronal nitric oxide synthase through alternative
                                                                                                                                                                                                                                                        MO)
                                                                                                                                                                                                                                                        ALTERNATIVE SPLICING (ISOFORMS NNOS BETA; NNOS GAMMA AND NNOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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Pfam; PF00595; PDZ; 1.
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InterPro; IPR001094; -.
InterPro; IPR001433; -.
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InterPro; IPR001709;
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CALMODULIN-BINDING (POTENTIAL).

FAM (PYRIMIDINE PART) (BY SIMILARITY).

FAD (ADP PART) (BY SIMILARITY).

FAD (RIDSE PART) (BY SIMILARITY).

NADP (RIBOSE PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).

NADP (AND PART) (BY SIMILARITY).

MISSING (IN ISOPORM NNOS BETA).

TGIOUD >> MRGIGS (IN ISOPORM NNOS BETA).

MISSING (IN ISOPORM NNOS GAMMA).

MISSING (IN ISOPORM NNOS GAMMA).
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                                                                                                                                    NNOS-INHIBITING PROTEIN (PIN)-BINDING (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillier B.J., Christopherson K.S., Prehoda K.E., Bredt D.S., Lim W.A.; "Unexpected modes of PDZ domain scaffolding revealed by structure of nNOS-syntrophin complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Magee T., Fuentes A.M., Garban H., Rajavashisth T., Marquez D., Rodriguez J.A., Rajfer J., Gonzalez-Cadavid N.F.; "Cloning of a novel neuronal nitric oxide synthase expressed in penis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> KYPEPLRFFPRKGPSLSHVDSEAHSLVAARDSOHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOS, TYPE I) (NEURONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cioned and expressed nitric oxide synthase structurally resembles cytochrome P-450 reductase.";
Nature 351:714-718(1991).
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MEDLINE-91287795; PubMed-1712077;
Bredt D.S., Hwang P.M., Glatt C.L., Lowenstein C., Reed R.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 78; DB 1; Length 1429;
Pred. No. 3.8e-05;
0; Mismatches 4; Indels
                 PROSITE; PSS0106; PD2; 1.
Oxidoreductase; NADP; FAD; FWN; Calmodulin-binding; Heme;
Alternative splicing; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3782848D65B41BFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOSI_RAT STANDARD; PRT; 1429 AA.
P29476; P70594;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
NITRIC-OXIDE SYNPHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE)
NOSI (N NOS) (NOS) (SNOS) (BNOS);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IN ISOFORM NNOS MU)
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STRAIN-FISCHER 344; TISSUE-Penis;
MEDLINE-96400229; Pubmed-8806605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99238815; PubMed=10221915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1429 AA; 160472 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.7%;
Best Logal Similarity 77.8%;
Matches 14; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GIVPFRSFWQORLHDSQH 18
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Science 284:812-815(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and lower urinary tract."
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1180
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                                                                                                                                    163
                                                                                                                                                                                                                                                                                                                            1245
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VARSPLIC
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                            HEME (BY SIMILARITY).

CALMODULIN-BINDING (POTENTIAL).

FAN (PYRINDINE PART) (BY SIMILARITY).

FAD (ADP PART) (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

NADP (RIBOSE PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).

MISSING (IN ISOFORM N'NOS-2).

K -> KYPEPLAFFPRKGPSLSHVDSEAHSLVAARDSQHR

(IN ISOFORM PINOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNOS-INHIBITING PROTEIN (PIN)-BINDING (BY
                     CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) - CITRULLINE +
PERIPHERAL NERVOUS SYSTEM, NO DISPLAYS MANY PROPERTIES OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase, NADP; FAD; FWN; Calmodulin-binding; Heme; Alternative splicing; Multigene family; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 1 -> V (IN REF. 2).
953 P -> A (IN REF. 2).
1008 F -> S (IN REF. 2).
1311 A -> V (IN REF. 2).
AA: 160559 MW; 7255C5AE165200F5 CRC64;
                                                                                                                                                                                                                                                           (BY SIMILARITY).
SIMILARITY: BELONGS TO THE NOS FAMILY.
SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00369; FLAVODOXIN
PRINTS; PR00371; FPNCR.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001094; -. InterPro; IPR001433; -. InterPro; IPR001478; -. InterPro; IPR001709; -.
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10AV; 06-MAR-00.
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"A novel, testis-specific mRNA transcript encoding an NH2-terminal
truncated nitric-oxide synthase.";
J. Biol. Chem. 272:11392-11401(1997).
-I- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN THE BRAIN AND
PERIPHERAL NERVOUS SYSTEM, NO DISPLAYS MANY PROPERTIES OF A
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM N-NOS-1).
MEDLINE-95105197; PubMed-7528745;
Hall A.V., Antoniou H., Wang Y., Cheung A.H., Arbus A.M., Olson S.L.,
Lu W.C., Kau C.-L., Marsden P.A.;
"Structural organization of the human neuronal nitric oxide synthase
gene (NOS1).";
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MEDLINE-97034095; PubMed-8879752;
Park C.-S., Glanotti C., Park R., Krishna G.;
"Neuronal isoform of nitric oxide synthase is expressed at low levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakane M., Schmidt H.H.H.W., Pollock J.S., Foerstermann U., Murad F.; "Cloned human brain nitric oxide synthase is highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE + TUTRIC OXIDE + N NADP(+).

COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                          Gaps
                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-007-1996 (Rel. 34, Last sequence update)
01-007-2000 (Rel. 40, Last annotation update)
NITRIC-OXIDE SYNTHANE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS).
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS TN-NOS; TN-NOSB AND TEX2 INSERTION)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Expression of two types of nitric oxide synthase mRNA in human neuroblastoma cell lines."; J. Neurochem. 63:140-145(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Cerebellum;
MEDLINE-94267447; PubMed-7515942;
Fujisawa H., Ogura T., Kurashima Y., Yokoyama T., Yamashita J.,
                                        .;
0
 Score 78; DB 1; Length 1429;
Pred. No. 3.8e-05;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS N-NOS-1 AND N-NOS-2).
                                                                                                                                                                                                   PRT; 1434 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in human retina.";
Cell. Mol. Neurobiol. 16:499-515(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blol. Chem. 269:33082-33090(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM N-NOS-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM N-NOS-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97269048; PubMed-9111048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93131039; PubMed-7678401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 316:175-180(1993).
 75.78;
77.88;
                                                                                           1 GIVPFRSFWQQRLHDSQH 18
                                     14; Conservative
                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEUROTRANSMITTER
Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain;
                                                                                                                                                                                               NOS1_HUMAN
P29475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Esumi H.;
                                                                                                                                                            RESULT 11
NOS1_HUMAN
                                                                                                          a
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JOINED. JOINED.

U17302; AAB60654.1 U17303; AAB60654.1 U17304; AAB60654.1

JOINED.

U17300; AAB60654.1 U17301; AAB60654.1

EMBL; EMBL; EMBL;

EMBL;

EMBL; U17327; AAA62405.1; U17299; AAB60654.1; JOINED. JOINED.

AAB60654.1 AAB60654.1

AAB60654

U17308;

EMBL; EMBL; EMBL; EMBL;

EMBL;

JOINED. JOINED. JOINED. JOINED. JOINED.

AAB60654.1; AAB60654.1; AAB60654.1; AAB60654.1;

JOINED

AAB60654.1; AAB60654.1;

U17313; 017314; 017315;

EMBL;

EMBL; EMBL; EMBL;

AAB60654.1; AAB60654.1;

AAB60654.1 AAB60654.1

JOINED. JOINED.

AAB60654.

U17318;

EMBL;

EMBL;

EMBL;

EMBL;

JOINED.

AAB60654.1;

AAB60654.1;

EMBL; EMBL;

EMBL;

EMBL; U66362; -; NOT_ANNOTATED_CDS. PIR; S28878; S28878. HSSP; P00388; 1AMO.

THE ENZYME.

L02881; AAA36376.1; U31466; AAB49040.1;

BAA03895

D16408

EMBL;

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THE SANCOLEMBE OF FASTITMITCH WOSCLE FIBER BY ASSOCIATING WITH THE DYSTROPHIN GIRCOPROTEIN COMPLEX.

1. ALTERNATIVE PRODUCTS: 4 ISOFORMS; N-NOS-1 (SHOWN HERE), N-NOS-2, TN-NOS/TN-NOSB AND TEXZ INSERTION; ARE PRODUCED BY ALTERNATIVE SPLICING. TN-NOS/TN-NOSB AND TEXE PRODUCED BY ALTERNATIVE SPLICING. TN-NOS/TN-NOSB AND THERE DEPERED EXONS TEXI (TN-NOS) OR TEXT TROUGHED EXONS TEXI (TN-NOS) OR TEXT TROUGHED PROTEIN WHICH POSSESSES ENZYMATIC ACTIVITY COMPARABLE TO THAT OF N-NOS-1. THE COH-TRUNCATED TEXZ INSERTION ISOFORM IS PRODUCED BY INSERTION OF THE TEXZ EXON BETWEEN EXONS 3 AND 4 OF THE N-NOS-1 ISOFORM, LEADING TO A FRAMESHIFT AND A PREMATURE STOP CODON.

1. TISSUE SPECIFICITY: THE N-NOS-1 ISOFORM IS UBIQUITOUSLY EXPRESSED: DEPECTED IN SKELFTAL MUSCLE AND BRAIN, ALSO IN TESTIS, LUNG AND KIDNEY, AND AT LOW LEVELS IN HEART, ADREAD, CLAND AND RETINA. NOT DETECTED IN THE PLATELETS. THE TN-NOS ISOFORM IS EXPRESSED ONLY IN THE TESTIS. THE TN-NOS ISOFORM IS DETECTED IN THE BRAIN, BUT NOT IN THE HEATEL TEXZ INSERTION ISOFORM IS DETECTED IN THE BRAIN BUT NOT IN THE HEATEL STOP IN THE BRAIN, BUT NOT IN THE HEATEN AND ADDREAD. GLAND.

1. DOMAIN: THE PDZ DOMAIN IN THE N-TERMINAL PART OF THE NEURONAL ISOFORM PARTICIPATES.

1. SOFORM PARTICIPATES IN PROTEIN-PROTEIN INTERACTION, AND IS EXPRESSED.

2. THE THERMAL AND RIDNEY, AT LOW EFFERS IN THE BRAIN, BUT NOT IN THE RESPONDED THE PROTEIN INTERACTION, AND ISOFORM PARTICIPATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outsition. The European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an emmail to licenseelsb-sib.ch).
                                                        SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: IN SKELETAL MUSCLE, IT IS LOCALIZED BENEATH
THE SARCOLEMMA OF FAST-TWITCH MUSCLE FIBER BY ASSOCIATING WITH THE
ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN. INHIBITED BY N-NOS-INHIBITING PROTEIN (PIN) WHICH MAY PREVENT THE DIMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE NOS FAMILY. SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                         OF THE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY
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11

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NP_BIND
NP_BIND
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NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPTSGKQSPTKNGSPSKCPRFLKVKNWETEVVLTDTLHLKS
TLETGCTEYICMGSIMHPSQHARRPEDVRTKGQLFPLAKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> MRKLRITEGFGVQRGSHNHPPPQENSPPQRMAAPPSVH
ASSRSRTGRLRWFSLIPSTLRAHWKRDALSTSAWAPSCILL
SWQGGLKTSAQKDSSSLSPKSLLINTIHQLKDLAPKPTWKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDQYYSSIKRFGSKAHMERLEEVNKEIDTTSTYQLKDTELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-96216113; PubMed-8662618;
Lin A.W., Chang C.C., McCormick C.C.;
"Molecular cloning and expression of an avian macrophage nitric-oxide synthase cDNA and the analysis of the genomic 5'-flanking region.";
J. Biol. Chem. 271:11911-11919(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                    CALMODULIN-BINDING (POTENTIAL).
FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
MADS (ADP PART) (BY SIMILARITY).
MISSING (IN ISOFORM TN-NOSE).
                                                                                                                                                                                                                                                                                    NNOS-INHIBITING PROTEIN (PIN)-BINDING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WKR (IN ISOFORM TEX2 INSERTION).
MISSING (IN ISOFORM TEX2 INSERTION).
MISSING (IN ISOFORM N-NOS-2).
K -> E (IN REF. 4).
LAPRPPG -> WPQAPR (IN REF. 3 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOS2_CHICK STANDARD, PRT; 1136 AA.
090703; 090677; 090934;
01.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
30-NAY-2000 (Rel. 39, Last annotation update)
NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
(INDUCIBLE NOS) (INOS) (MACROPHAGE NOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                       PRINTS; PRO0369; ELAVODOXIN.
RPRINTS; PR00371; FPNCR.
R PROSITE; PS00106; PDZ; 1.
W Alternative splicing; Multigene family.
W Alternative splicing; Multigene family.
DOMAIN 163 245 HEME (BY SIMILARITY).
T DOMAIN 163 245 HEME (BY SIMILARITY).
T DOMAIN 730 750 CALMODDIIN BINDING (POTENTIAL).
T DOMAIN 730 750 CALMODDIIN BINDING (POTENTIAL).
T NP_BIND 886 917 FWN (PYRIMIDINE PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99235793B953BF37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QP -> HR (IN REF. 3).
V -> L (IN REF. 3).
G -> A (IN REF. 3).
Y -> I (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 78; DB 1; I
Pred. No. 3.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
         InterPro; IPR001094; -.
InterPro; IPR00143; -.
InterPro; IPR001478; -.
InterPro; IPR001478; -.
InterPro; IPR001709; -.
InterPro; IPR003097; -.
Pfam; PF00657; PAD_binding; 1.
Pfam; PF00555; PDZ; I.
Pfam; PF00175; oxidored_fad; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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77.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIVPFRSFWQQRLHDSQH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613
131
184
493
549
563
                                                                                                                                                                                                                                                                                                                                                           1043
11185
1268
1363
336
407
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOS2_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in chick embryonic ventricular myocytes.";
Cardiovasc. Res. 38.405-413(1998).
-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. NO MAY SERVE AS BOTH A PARACRINE AND AUTOCRINE SIGNAL FOR MODULATING OSTEOCLAST BONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:-CATALTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE + NITRIC OXIDE + N NADP(+).

-:-COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF THE ENZYME (BY SIMILARITY).

-:-ENZYME (BY SIMILARITY).

-:-CUBGUITT: HOMODIMER (BY SIMILARITY).

-:-CUBGUITT: HOMODIMER (BY SIMILARITY).

-:-CUBGUITT: HOMODIMER (BY SIMILARITY).

-:-CUBGUITT: HOMODIMER (BY SIMILARITY).

-:-CALCIUM AND PMA (PHORBOL 12-MYRISTATE THEY ARE INDUCED BY CALCIUM AND PMA (PHORBOL 12-MYRISTATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEME (BY SIMILARITY).
CALMODULIN-BINDING (POTENTIAL).
FAM (PYRINIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
                                                         TISSUE-Osteoclast;
MEDLINE-96252270; PubMed-8707887;
Sunyer T., Rothe L., Jiang X., Osdoby P., Collin-Osdoby P.;
"Proinflammatory agents, IL-8 and IL-10, upregulate inducible nitric oxide synthase expression and nitric oxide production in avian
                                                                                                                                                                                                                                                                                                                                                                                                                   Shimizu T., Kinugawa K., Sugishita Y., Sugishita K., Harada K.,
Matsui H., Kohmoto O., Serizawa T., Takahashi T.;
"Molecular cloning and expression of inducible nitric oxide synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S -> T (IN REF. 2).
R -> S (IN REF. 3).
MW; D5CB73AC7BA94B9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 76; DB 1; Pred. No. 6.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                       J. Cell. Biochem. 60:469-483(1996).
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98375063; PubMed=9709401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR003097; --
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
PRINTS; PR00365; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 646-986 FROM N.A.
[2]
SEQUENCE OF 171-472 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U46504; AAC59886.1; -. EMBL; U34045; AAB17499.1; -. EMBL; D85422; BAA12817.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.8%;
86.7%;
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Best Local Similarity 86./۳,
دمه 13; Conservative
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NOS3_HUMAN STANDARD; PRT; 1202 AA.
P29474, Q14251; Q14643; Q13662;
01-APR-1993 (Rel. 25, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC-OXIDE SYNTHASE, ENDOTHELIAL (EC 1.14.13.39) (EC-NOS) (NOS, TYPE III) (NOSIII) (ENDOTHELIAL NOS) (ENOS) (CONSTITUTIVE NOS) (CNOS).
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-92340475; PubMed-1378832;
Janssens S.P., Shimouchi A., Quertermous T., Bloch D.B., Bloch K.D.;
"Cloning and expression of a cDNA encoding human endothellum-derived relaxing factor/nitric oxide synthase.";
J. Biol. Chem. 267:14519-14522(1992).
                                                                                                                                                                                                                                                                                                                        Bloch K.D.;
                                                                                                                                                                                                                                                                                                                                                                             Marsden P.A., Schappert K.T., Chen H.S., Flowers M., Sundell C.L., Wilcox J.N., Lamas S., Michel T.; "Molecular cloning and characterization of human endothelial nitric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endothelial
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MADLINE-93352539; PubMed-7688726;
MATSGEN P.A., Heng H.H., Scherer S.W., Stewart R.J., Hall A.V.,
Shi X.M., Tsui L.C., Schappert K.T.;
Structure and chromosomal localization of the human constitutive
endothelial nitric oxide synthase gene.";
J. Biol. Chem. 268:17478-17488(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-9433373; PubMed=7519987;
Miyahara K., Kawamoto T., Sase K., Yui Y., Toda K., Yang L.X.,
Miyahara R., Rawamoto T., Sase K., Doi Y., Ogoshi S.,
Hattori R., Aoyama T., Yamamoto Y., Doi Y., Ogoshi S.,
Hashimoto K., Kawai C., Sasayama S., Shizuta Y.;
"Cloning and structural characterization of the human endothelial
                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                       Biol. Chem. 267:22694-22694(1992).
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Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nadaud S.A., Bonnardeaux A., Lathrop M., Soubrier F., "Gene structure, polymorphism and mapping of the human nitric oxide synthase gene.";
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Eur. J. Biochem. 223:719-726(1994).
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92354731; Pubmed-1379542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94161710; PubMed-7509596;
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TISSUE-Placenta;
MEDLINE-94245207; Pubmed-7514568;
                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett. 307:287-293(1992).
                      15
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TISSUE=Umbilical vein;
         1 GIVPFRSFWQQRLHD
                                                                                                                                                                            Homo saptens (Human)
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collaboration MEDLINE-96077182; PubMed-7475956; Sase K., Michel T.; "Expression of constitutive endothelial nitric oxide synthase in human blood platelets."; "A missense Glu298Asp variant in the endothelial nitric oxide synthase -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) & CITRULLINE + N NTRIC OXIDE + N NADP(+).

NITRIC OXIDE + N NADP(+).

-1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILLIZE THE DIMERIC FORM OF VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A CGMP-MEDIATED SIGNAL TRANSPUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH FACTOR (VECF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS. MDDLINE-08407797; Probector of Types of X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).

BUDLINE-99173237, PubMed-in0074942;
Fischmann T.O., Hruza A., Niu X. D., Fossetta J.D., Lunn C.A.,

Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K., Robinson L.J., Weremowicz S., Morton C.C., Michel T.; "Isolation and chromosomal localization of the human endothelial FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN "Structural characterization of nitric oxide synthase isoforms reveals striking active-site conservation."; Nat. Struct. Biol. 6:233-242(1999). THE ENZYME.
--- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN.
--- SUBUNTY: HOMODIMER.
--- TISSUE SPECIFICITY: PLATELETS.
---- DISEASE: DEFECTS IN NOS3 ARE INVOLVED IN CORONARY SPASM.
--- SIMILARITY: BELONGS TO THE NOS FAMILY. gene is associated with coronary spasm in the Japanese."; Hum. Genet. 103:65-69(1998). nitric oxide synthase (NOS3) gene." Genomics 19:350-357(1994). JOINED. JOINED. JOINED JOINED JOINED JOINED JOINED JOINED JOINED. VARIANT CORONARY SPASM ASP-297 Life Sci. 57:2049-2055(1995). SEQUENCE OF 410-527 FROM N.A. EMBL; M93718; AAA36364.1; -. L10709; AAA36365.1; L10693; AAA36365.1; L10694; AAA36365.1; L10695; AAA36365.1; L10697; AAA36365.1; AAA36365.1; AAA36365 M95296; AAA36372 AAA36365 TISSUE-Platelet; L10701; L10703; L10700; L10707 Nakao K EMBL; EMBL;

AAA36365.1;

L10708;

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III) (NOSIII) (ENDOTHELIAL NOS) (ENOS) (CONSTITUTIVE NOS) (CNOS).
NOS3.
                                                                                   Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                       taurus (Bovine).
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30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC-OXIDE SYNTHASE, ENDOTHELIAL (EC 1.14.13.39) (EC-NOS) (NOS, TYPE
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FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
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FAD (ADP PART) (BY SIMILARITY)
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
MADP (ADP PART) (BY SIMILARITY).
MYRISTATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;
Lipoprotein; Palmitate; Disease mutation; Calcium-binding; Heme;
Zinc; Metal-binding; Multigene family; 3D-structure.
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93D127D6C14AC92E CRC64;
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E -> D (IN CORONARY SI / FIId=vAR_008037.
S -> K (IN REF. 8).
G -> S (IN REF. 9).
V -> W (IN REF. 6).
R -> RO (IN REF. 6).
R -> RO (IN REF. 6).
C -> E (IN REF. 6).
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Pred. No. 0.0001;
1; Mismatches 2
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NOS3_BOVIN

1029473;

01-APR-1993 (Rel. 25, Created)

01-JUL-1993 (Rel. 26, Last seque

01-JUL-1993 (Rel. 39, Last annot

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Pfam; PF00175; oxidored_fad; 1.
PRIWES; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
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80.0%;
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CAA53950.1;
CAA53950.1;
CAA53950.1;
CAA53950.1;
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BAA05652.1;
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CAA53950.1;
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CAA53950.1;
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Best Local Similarity 80.0
Matches 12; Conservative
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InterPro; IPR001433; -.
InterPro; IPR001709; -.
InterPro; IPR003097; -.
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A42867; A42867
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X76308;
X76309;
X76310;
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PIR; A42867;
PDB; 3NOS; 04
MIM; 163729;
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VARIANT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation for European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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TISSUE-AOTLIC endothelium;
MEDLINE-92348367; PubMed=1379225;
Sessa W.C., Harrison J.K., Barber C.M., Zeng D., Durieux M.E.,
D'Angelo D.D., Lynch K.R., Peach M.J.;
"Molecular cloning and expression of a cDNA encoding endothelial cell
nitric oxide synthase.";
J. Biol. Chem. 267:15274-15276(1992).
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-!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
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MEDLINE=99091052; PubMed=9875848;
Raman C.S., Li H., Martasek P., Kral V., Masters B.S., Poulos T.L.;
"Crystal structure of constitutive endothelial nitric oxide synthase: a paradigm for pterin function involving a novel metal center.";
Cell 95:939-950(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robinson L.J., Michel T.; "Mutagenesis of palmitoylation sites in endothelial nitric oxide synthase identifies a novel motif for dual acylation and subcellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MISDLINE-99055452;
MISDLINE-99055452;
MISDLINE-99055452;
MISDLINE-901054;
MARCHAR K., HARTISON D.G., NAVAS J.P., Fisher A.A., Dockery S.P., Uematsu M., Nerem R.M., Alexander R.W., Murphy T.J.;
Misolecular cloning and characterization of the constitutive bovine acrtic endothalial cell nitric oxide synthase.";
J. Clin. Invest. 90:2092-2096(1992).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .i. FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-92335295; PubMed=1378626;
Lamas S., Marsden P.A., Li G.K., Tempst P., Michel T.;
Lamothelial nitric oxide synthase: molecular cloning and
characterization of a distinct constitutive enzyme isoform.";
Proc. Natl. Acad. Sci. U.S.A. 89:6348-6352(1992).
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MEDLINE-93231982; PubMed-7682550;
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0289667
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
10TRIC-OXIDE SYMTHASE, ENDOTHELIAL (EC 1.14.13.39) (EC-NOS) (NOS, TYPE III) (NOSIII) (ENDOTHELIAL NOS) (ENOS) (CONSTITUTIVE NOS) (CNOS).
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CALMODULIN-BINDING (POTENTIAL).
FEM (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
FAD (RIBOSE PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (P1g).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                                                                            REF.
                                                                                                                                                           Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate; Lipoprotein; Palmitate; Phosphorylation; Calcium-binding; Heme; Zinc; Metal-binding; Multigene family; 3D-structure.
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Y -> I (IN REF. 3).
Y -> Y (IN REF. 3).
EHPTLEWFAAL -> GAPHTGVVRGP (IN RE S. -> Y (IN REF. 3).
T -> P (IN REF. 3).
CP -> SA (IN REF. 3).
CP -> SA (IN REF. 3).
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WF -> L (IN REF. 3).
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> H (IN REF. 3).
D017210062ABE4B0 CRC64;
                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY CAPK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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PALMITATE.
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or send an email to license@isb-sib.
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                                            PDB: 1NSE; 18-MAY-99.
PDB: 2NSE; 25-MAY-99.
PDB: 3NSE; 18-MAY-99.
PDB: 4NSE; 18-MAY-99.
InterPro: 1PR001094; -.
InterPro: 1PR0011094; -.
InterPro: 1PR0011094; -.
InterPro: 1PR001109; -.
InterPro: PR001709; -.
Pfam: PF00667; FAD_binding; 1.
Pfam: PF000175; oxidored_fad; 1.
PRINTS; PR00175; radoved_fad; 1.
PRINTS; PR00371; FPNCR.
                 EMBL; M99057; AAA30667.1; -. EMBL; M89952; AAA30494.1; -. EMBL; M95674; AAA30669.1; -.
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-97293429; PubMed-9149402; Zhang J., Patel J.M., Block E.R.; Zhang J., Patel J.M., Block E.R.; Molecular cloning, characterization and expression of a nitric oxide synthase from porchine pulmonary artery endothelial cells."; Comp. Blochem. Physiol. 1168:485-491(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).

-1. CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) & CITRULLINE + NITRIC OXIDE + N NADP(+).

-1. COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBLOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF THE ENZYME (BY SIMILARITY).

-1. ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEME (BY SIMILARITY).

CALMODULIN BINDING (POTENTIAL).

FAN (PYRINDINE PART) (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).

MYRIGTATE (BY SIMILARITY).

PALMITATE (BY SIMILARITY).

PALMITATE (BY SIMILARITY).

ZINC (BY SIMILARITY).

ZINC (BY SIMILARITY).
                                                                                                                                                                                                                              Patel J.M., Block E.R.;
Submitted (Aug-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN
VASCULAR SWOOTH MUSCLE RELAXATION THROUGH A CGMP-MEDIATED SIGNAL
TRANSDOCTION PATHWAY. NO MEDIATES VASCULAR ENDOYTHELIAL GROWTH
FACTOR (VEGP)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND
PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Lipoprotein; Palmitate; Calcium-binding; Heme; Zinc; Metal-binding;
Multigene family.
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Pred. No. 0.0001;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
-1- INDUCTION: REPRESSED BY PROINFLAMMATORY CYTOKINES.
-1- SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
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InterPro; IPR001094; --
InterPro; IPR001433; --
InterPro; IPR001709; --
Pfam; PF00667; FAD_binding; 1.
Pfam; PR00175; oxidored_fad; 1.
PRINTS; PR00359; FLAVDDOXIN.
                                                                                                                                                                    [2] SEQUENCE OF 1031-1205 FROM N.A.
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80.0%;
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Matches 12; Conser
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Search completed: September 10, 2001, 14:09:51 Job time: 560 sec

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GenCore version 4.5
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gen Ltd.		<pre>: Search time 42.28 Seconds (without alignments) 32.430 Million cell updates/sec</pre>
Copyright (c) 1993 - 2000 Compugen Ltd.	OM protein - protein search, using sw model	September 10, 2001, 13:57:41; Search time 42.28 Seconds (without alignments) 32.430 Million cell updates.
	OM protein -	Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 GIVPFRSFWQORLHDSQH 18 US-08-833-506C-25 103 Title: Perfect score: Scoring table: Sequence:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

219241

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:* pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ic-oxide sy	nitric-oxide synth		nitric-oxide synth			nitric-oxide synth			nitric-oxide synth	nitric-oxide synth	nitric-oxide synth	nitric-oxide synth	sulfite reductase	sulfite reductase	sulfite reductase	hypothetical prote	ferredoxinNADP+	ferredoxinNADP+										
SUMMARIES	ID	A43271	S47647	156575	S38253	JC5027	JC5028	JC5029	S65440	A49676	153165	139204	146074	JN0609	S16233	G01946	A47501	A38943	S71424	T31080	151917	T31331	T30555	25		A34231	H65057	D85926	S72222	80
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	Score	66	66	66	66	66	66	66	66	66	91	86	79	78	78	78	75	75	73	69	63	57	26	26	53	25	52	52	51	51
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C83919	G70040	AB3726	B82329	T14904	T10723	S37156	T50103	S37157	E81905	н81110	S37159	T14081	S21531	JE0230	S31502
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47.6	46.6	46.6	45.6	45.6	45.6	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7
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30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT

-	A43271	
-	nitric-oxide synthase (EC 1.14.13.39), calmodulin-independent	1.14.13.39), calmodulin-independent - mouse
-	C; Species: Mus musculus (house mouse)	onse mouse)
	C;Date: 10-Sep-1999 #sequence_revision 10-Sep-	C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Mar-2000
	Divid O Chaccession: A432/1; A42100; UNU430; A40100	0; UNU436; A46160 most I : Minford D A : Cuidotek K M : Ioo I D : Ding A
	Science 256, 225-228, 1992	N. N. Saturday, N. H. J. Book I. D. J. Bring,
	A; Title: Cloning and characterization of induc	A, Title: Cloning and characterization of inducible nitric oxide synthase from mouse m
	A; Reference number: A43271; MUID:9229444	; MUID:9229444
	A; Accession: A43271	
-	A;Status: preliminary	
	A; MOLECULE LYPE: MINNA A: Residues: 1-1144 <xte></xte>	
	A; Cross-references: GB: M87039; NID:q198406; PIDN: AAA39315.1; PID:q198407	039; NID:q198406; PIDN:AAA39315.1; PID:g198407
	R; Lyons, C.R.; Orloff, G.J.; Cunningham, J.M.	.; Cunningham, J.M.
_	Biol. Chem. 267, 6370-6374, 1992	
	A; Title: Molecular cloning and functional expr	and functional expression of an inducible nitric oxide syn
	A: Accession: A42166	0.1001.322.0010
	A:Status: preliminary	
	A; Molecule type: mRNA	
	A; Residues: 1-1144 <lyo></lyo>	
	A;Cross-references: GB:M84373; NID:g200095; PI	A;Cross-references: GB:M84373; NID:g200095; PIDN:AAA39834.1; PID:g200096
		H.; Sherman, P.A.; Lapetina, E.G.
	Biochem. Biophys. Res. Commun. 191, 767-774, 1	1993
	ess	acrophages express an identical cytokine inducible nitric o
	A: Acceptance number: JNU45/; MUID: 93221515	CTCT7766:ATOW :
_	A; Accession: JN0458	minds to account
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	A; Residues: 1-278, F', 280-682, H', 684-937, 939-1144 <woo></woo>	682,'H',684-937,939-1144 <woo></woo>
	A; Experimental source: liver	าอ
	R; Lowenstein, C.J.; Glatt, C.S.; Bredt, D.S.; Snyder,	C.S.; Bredt, D.S.; Snyder, S.H.
	Proc. Natl. Acad. Sci. U.S.A. 89, 6711-6715, 1	.A. 89, 6711-6715, 1992
_	A; Title: Cloned and expressed macrophage nitri	A; Title: Cloned and expressed macrophage nitric oxide synthase contrasts with the bra
	A; Reference number: A46186; MUID: 92357701	; MUID:92357701
	A ACCESSION: A 440 LBC A CTAILE TO A COLORATION THE COMMONDER OF THE COLORATION T	compared with conceptual translation
	A: Molecule type: mRNA	Compared *Itil Collegetage cranstaction
	A; Residues: 1-190, 'V', 192-765, 'P', 767-843, 'G', 845-1144 <low></low>	765,'P',767-843,'G',845-1144 <low></low>
	A;Cross-references: GB:M92649; NID:9200109	649; NID:9200109
	A; Experimental source: BALB/c, RAW 264.7 cells	B/c, RAW 264.7 cells, macrophage
	A; Note: sequence extracted from NCBI backbone (NCBIP:113541)	from NCBI backbone (NCBIP:113541)
_	C; Genetics:	
	A; Gene: NOS	
_	C;Function:	
_	A; Description: Catalyzes the Oxidation of an L	A) Description: catalyzes the oxidation of an in-arginine quantianno introgen and or NAD
	C;Superiamily: nitric-oxide synthase; ilavodox	C.Suberramily: hittic-oxide Sylutase; ilavodoxin homology; nauven-terinemopiotein fe C.Kouronde: ozalmodulia bindinar chromonortein: Edb. flanorotein: EMN. heme: from me
_	C. Neywolds. Calmondain Binding, CHIOUDIOCETH, FAD, HIAVOLIN, E. 523-1121 (December of the Computer of the Com	fornibomomnotoin reductase homology (PRU)
_		in homology <flx></flx>
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R;Tsutsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa Biol. Pharm. Bull. 19, 1374-1376, 1996
A;Titles Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, an A;Teference number: JC5027; MUID:97070590
A;Accession: JC5027
A;Accession: JC5027
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 1-1147 <FTSU>
A;Estidues: 1-1147 <FTSU
A;Estidues: 1-1147 <FTSU>
A;Experimental source: kidney
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein rec;Reywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FNN; heme; iron; me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Experimental source: liver
R; Wood, E. R.; Barger Jr., H.; Sherman, P.A.; Lapetina, E.G.
Biochem. Blophys. Res. Commun. 191, 767-774, 1993
A; Title: Hepatocytes and macrophages express an identical cytokine inducible nitric of A; Reference number: JN0457; MUID:93221515
A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                      nitric-oxide synthase (EC 1.14.13.39) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Dacession: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Jun-2000
C;Accession: S38253; JN0457
R;Adachi, H.; Idda, S.; Oquchi, S.; Ohshima, H.; Suzuki, H.; Nagasaki, K.; Kawasaki,
Eur. J. Blochem. 217, 37-43, 1993
A;Title: Molecular cloning of a cDNA encoding an inducible calmodulin-dependent nitri
A;Reference number: S38253; MUID:94039059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NAD C; Superfamily: nitric-oxide syrthase; flavodoxin homology; NADPH--ferrihemoprotein re C; Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me F; 536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Wolecule type: mRNA
A;Residues: 1.41,'SS',44-103,105-190,'Q',192-213,'R',215-247,'T',249-263,'I',265-373,
'S',896-1000,'LG',1003-1015,'RR',1018-1026,'EQ',1029-1147 <WOO>
A;Cross-references: PIDN:AAB26037.1
A;Experimental source: liver
C;Genetics:
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                                                                                                                         Gaps
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A;Residues: 1-1147 <ADA>
A;Cross-references: GB:D12520; NID:9391858; PIDN:BAA02090.1; PID:9391859
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                                     Length 1147;
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Score 99; DB 1; Ler
Pred. No. 8.2e-08;
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94.4%; Pred No 8.2e-08;
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C;Species: Rattus norveglcus (Norway rat)
C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997
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                                     96.1%;
94.4%;
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Best Local Similarity 94.4'
Matches 17; Conservative
                                                                                                                    Conservative
                                                                           Best Local Similarity
Matches 17; Conserv
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                                     Query Match
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347647
nitric-oxide synthase (EC 1.14.13.39) - rat
c.:Species: Rattus norvegicus (Norway rat)
C.:Date::20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Jun-2000
C.:Accession: 847647; JC1472
R.:Geng, Y.: Almqvist, M.: Hansson, G.K.
Biochim. Biophys. Acta 1218, 421-424, 1994
A.Title: CDNA cloning and expression of inducible nitric oxide synthase from rat vascula A; Reference number: 847647; MUID:9432551
A.Accession: 847647
A.Molecule type: mRNA
A.Residues: 1-1147 <GENA
A.Molecule type: mNA
A.Residues: 1-1147 <GENA
A.Molecule type: mNA
A.Residues: 1-117 Y.Y. 73-347, PVV, 350-678, VPV, 681-720, 'L',722-739, 'L',741-843, 'G',845-1C
A.Molecule type: DNA
A.Residues: 1-71, YY, 73-347, 'PVV, 350-678, 'VPV, 681-720, 'L',722-739, 'L',741-843, 'G', 845-1C
A.Cross-references: DNA
A.Residues: 1-71, YY, 73-347, 'PVV, 350-678, 'VPV, 681-720, 'L',722-739, 'L',741-843, 'G', 845-1C
A.Cross-references: DNA
A.Residues: 1-71, YY, 73-347, 'PVV, 350-678, 'VPV, 681-720, 'L',722-739, 'L',741-843, 'G', 845-1C
A.Cross-references: DNA
A.Residues: 1-71, YY, 73-347, 'PVV, 350-678, 'VPV, 681-720, 'L',722-739, 'L', 741-843, 'G', 845-1C
A.Cross-references: DNA
A.Residues: 1-71, YY, 73-347, 'PVV, 350-678, 'VPV, 681-720, 'L',722-739, 'L', 741-843, 'G', 845-1C
A.Cross-references: DNA
A.Residues: 1-71, YY, 73-347, 'PVV, 350-678, 'VPV, 681-720, 'L',722-739, 'L', 741-843, 'G', 845-1C
A.Cross-references: DNA
A.Residues: 1-71, YY, 73-347, 'PVV, 350-678, 'PVP, 681-720, 'L',722-739, 'L', 741-843, 'G', 845-1C
A.Cross-references: DNA
A.Residues: 1-71, YY, 73-347, 'PVV, 350-678, 'PVP, 681-720, 'L',722-739, 'L', 741-843, 'G', 845-1C
A.Cross-references: DNA
A.Residues: 1-71, YY, 73-347, 'PVV, 350-678, 'PVP, 681-720, 'L',722-739, 'L', 741-843, 'G', 845-1C
A.Cross-references: DNA
A.Residues: 1-71, YY, 73-747, 'PVP, 'RVP, 
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Sattus norvegicus (Norway rat)
C;Species: Reis, D.J; Feinstein, D.L.
J. Neurosci. Res. 37, 406-444, 1994
A;Title: Cloning and expression of inducible nitric oxide synthase from rat astrocytes.
A;Reference number: 156575; MUID:94231594
A;Title: Cloning and expression of inducible nitric oxide synthase from rat astrocytes.
A;Reference number: 156575; MUID:94231594
A;Retaus: translated from GB/EMBL/DDBJ
A;Retaus: translated from from Cys) (axial ligand) #status predicted
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Pred. No. 8.2e-08;
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ilarity 94.4%;
Conservative
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Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
Matches 17; Conserv
                             F;194/Binding site:
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Cypaces, 20 Cut. 1750 (1964)

R. Iwashina, M.; Hirata, Y.; Imai, T.; Sato, K.; Marumo, F.

R. Iwashina, M.; Hirata, Y.; Imai, T.; Sato, K.; Marumo, F.

R. Iwashina, M.; Hirata, Y.; Imai, T.; Sato, K.; Marumo, F.

R. Jalochem. 237, 668-673, 1996

A. Title: Molecular cloning of endothelial, inducible nitric oxide synthase gene from A; Reference number: S65440

A. Accession: S65440

A. Accession: S65440

A. Status: not compared with conceptual translation
A; Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
C; Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reductase homology cFEH>
C; Superfamily: nitric-oxide synthase; flavodoxin homology cFEH>
F; 566-535 Region: calmodulin binding
F; 556-1124/Domain: NADPH--ferrihemoprotein reductase homology cFEH>
F; 539-618 Region: biopterin binding
F; 539-618 Region: biopterin binding #status predicted
F; 764-775/Region: PAD binding #status predicted
F; 764-775/Region: PAD binding #status predicted
F; 764-775/Region: NADPH binding #status predicted
F; 767-993/Region: NADPH binding #status predicted
F; 1074-1087/Region: NADPH binding #status predicted
F; 1077-1087/Region: NADPH binding #status predicted
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Cipecies: Homo sapiens (man)
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Cipecies: A49676; MulD:94068614
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A;Molecule type: mRNA
A;Residues: 1.607, 'L',609-1153 <H0K>
A;Cross-references: D091:D26525; NID:9559326; PIDN:BAA05531.1; PID:91228940
A;Experimental source: glioblastoma cell line A-172
R;Park, R; Park, R; Krishna, G.
submitted to the EMBL Data Library, July 1995
A;Reference number: G08912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
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Pred. No. 8.2e-08;
0; Mismatches 1; Indels
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           Score 99; DB 2; Pred. No. 8.2e-08;
                                                                                                                         0; Mismatches
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           96.18;
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Matches 17; Conservative
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                                                                                                                                    Conservative
                 Query Match
Best Local Similarity
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C; Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 04-Mar-2000
C; Accession: JC5028
R; Tsutsumishita, Y:; Kawai, Y:; Takahara, H:; Onda, T:; Miyoshi, J:; Futaki, S.; Niwa, M Biol. Pharm. Bull. 19, 1374-1376, 1996
A; Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and u A; Reference number: JC5027; MUID:97070590
A; Accession: JC5028
A; Accession: JC5028
A; Accession: JC5028
A; Accession: JC5028
A; Residues: 1-1147 <-TSU>
A; Residues: 1-1147 <-TSU
A; Res
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C; Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 04-Mar-2000
C; Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 04-Mar-2000
C; Accession: JC5029
R; Tsutsumishita, Y; Kawai, Y; Takahara, H; Onda, T; Miyoshi, J.; Futaki, S.; Niwa, M Biol. Pharm. Bull. 19, 1374-1376, 1996
A; Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and u A; Reference number: JC502; MUD: 97070590
A; Reference number: JC5029
A; Status: nucleic acid sequence not shown
A; Molecule type: MRNA
A; Residues: 1-1147 <TSU>
A; Residues: 1-1147 <TSU
A; Residues: 1-114
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F;191-199/Domain: heme-binding #status predicted <HMD>
F;536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>
F;538-674/Domain: flavodoxin homology <FLX>
F;620-647/Domain: FMN binding #status predicted <FMN>
F;764-775,899-910/Domain: FAD binding #status predicted <FAN>
F;764-775,899-910/Domain: RAD binding #status predicted <NDP>
F;975-993,1054-1067/Domain: NADP binding #status predicted <NDP>
F;197/Binding site: heme iron (Cys) (axial ligand) #status predicted
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94.4%; Pred. No. 8.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 99; DB 2;
Pred. No. 8.2e-08;
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94.4%;
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Best Local Similarity 94.4
Matches 17; Conservative
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Best Local Similarity 94.4
Matches 17; Conservative
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Gaps

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Length 1147;

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nitric-oxide synthase (EC 1.14.13.39) 2C - human (fragment)
N;Alternate names: nitric oxide synthase II
C;Species: Homo saplens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 11-Jun-1999
C;Accession: I39204
R;Bloch, K.D.; Wolfram, J.R.; Brown, D.M.; Roberts, J.D.
Genomics 27, 526-530, 1995
A;Title: Three members of the nitric oxide synthase II gene family (NOS2B, and A;Reference numbers. A57622; MUID:96047340
A;Accession: I39204
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R; Bloch, K.D.; Wolfram, J.R.; Brown, D.M.; Roberts, J.D.
Genomics 27, 526-530, 1995
A; Title: Three members of the nitric oxide synthase II gene family (NOS2A, NOS2B, and A; Reference number: A57622; MUID:96047340
                                              A; Molecule type: mRNA
A; Residues: 1-1147 < RES>
A; Cross-references: EMBL:U26686; NID:9886072; PIDN:AAA85861.1; PID:9886073
A; Cross-references: EMBL:U26686; NID:986072; PIDN:AAA85861.1; PID:9886073
A; Genetics:
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: C; Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein C; Reywords: calmodulin binding; chromoprotein; FAD; flavoprotein; ENN; heme; iron; F; 536-1124/Domain: NADPH--ferrihemoprotein reductase homology < FEH>
F; 536-1124/Domain: flavodoxin homology < FLX>
F; 538-674/Domain: flavodoxin homology < FLX>
F; 197/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 17p13.1-17q25
A;Introns: 33/1
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein
C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U18335; NID:g1050946; PIDN:AAC50245.1; PID:g1050948
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U18331; NID:g1041681; PIDN:AAC48479.1; PID:g1041682 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 91; DB 1; Length 114
Pred. No. 1.6e-06;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nitric-oxide synthase (EC 1.14.13.39) II - bovine (fragment)
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Pred. No. 5.1e-07;
0; Mismatches 2;
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A;Cross-references: GDB:547943; OMIM:600720
                          translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                            88.3%;
94.1%;
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88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 88.3
Best Local Similarity 94.1
Matches 16; Conservative
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Matches 15; Conservative
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A; Residues: 1-136 <BLO>
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A; Accession: G01947
A; Access
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153165
nitric-oxide synthase (EC 1.14.13.39) [similarity] - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C;Accession: 153165
R;Karlsen, A.E.; Andersen, H.U.; Vissing, H.; Larsen, P.M.; Fey, S.J.; Cuartero, Diabetes 44, 753-758, 1995
A;Title: Cloning and expression of cytokine-inducible nitric oxide synthase cDNA A;Reference number: 153165; MUID:95309542
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Pred. No. 8.2e-08;
0; Mismatches 1;
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94.48;
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Best Local Similarity
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Length 69; Indels S

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A. Molecule type: protein
A. Residues: 119-129:132-147:144-156;189-200;264-268, 'V', 270-276;305-310;360-369;376-3
A. Residues: 119-129:132-147:144-156;189-200;264-268, 'V', 270-276;305-310;360-369;376-3
A. Experimental source: colorectum
C. Comment: This protein is a cell signaling agent in the cardiovascular, central and
C. Superfamily: GLGF domain homology; flavodoxin homology; NADPH--ferrihemoprotein red
C. Superfamily: GLGF domain homology clambding chromoprotein; flavoprotein; heme; if
C. S. 3-95, Domain: CLGF domain homology clambding status predicted
F. 755-745/Region: calmodulin binding #status predicted
F. 755-1394/Domain: NADPH--ferrihemoprotein reductase homology cFEH>
F. 755-1394/Domain: RabPH--ferrihemoprotein reductase homology cFEH>
F. 757-315/Region: PMD binding #status predicted
F. 1077-1038/Region: NADP binding #status predicted
F. 1245-1263/Region: NADP binding #status predicted
F. 1245-1263/Region: NADP binding #status predicted
F. 1245-1263/Region: NADP binding #status predicted
F. 1545-1263/Region: NADP binding #status predicted
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A Status: preliminary; translated from GB/EWBL/DDBJ
A Status: preliminary; translated from GB/EWBL/DDBJ
A Molecule type: mRNA
A Mesidues: 1-130, "K'.132-177, "LA',179," RP',182,"G',184-1433 <RES>
A; Cross-references: GB:D16408; NID:9506339; PIDN:BAA03895.1; PID:9987662
A; Cross-references: GB:D16408; NID:9506339; PIDN:BAA03895.1; PID:9987662
A; Nakane, M.; Schmidt, H.H.H.W.; Pollock, J.S.; Foerstermann, U.; Murad, F.
A; Nakane, M.; 175-180, 1993
A; Title: Cloned human brain nitric oxide synthase is highly expressed in skeletal mus
A; Reference number: S28878; MUID:93131039
                                                                                                                                               R;Seo, H.G.; Tatsumi, H.; Fujii, J.; Nishikawa, A.; Suzuki, K.; Kangawa, K.; Taniguch J. Biochem. 115, 602-607, 1994
A;Title: Nitric oxide synthase from rat colorectum: Purification, peptide sequencing, A;Reference number: PC2184; MUID:94334309
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A;Map position: 12q24.2-12q24.31
C;Superfamily: GLGF domain homology; flavodoxin homology; NADPH--ferrihemoprotein red
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-130,′K′,132-490,′HR′,493-547,′L′,549-561,′A′,563-1362,′I′,1364-1405,′I′
A;Cross-references: GB:L02881; NID:g189261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1433 <PABN:
A;Cross-references: EMBL: U31466; NID:g951318; PIDN:AAB49040.1; PID:g951319
R;Fujisawa, H.; Ogura, T.; Kurashima, Y.; Yokoyama, T.; Yamashita, J.; Esumi, H.
J. Neurochem. 63, 140-145, 1994
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C;Date: 21-Dec.1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
C;Accession: 601946; 155608; $28878
R;Park, C.; Glanotti, C.; Park, R.; Krishna, G.
submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nitric-oxide synthase (EC 1.14.13.39), neuronal - human N;Alternate names: nitric oxide synthase 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.7%; Score 78; DB 2; 1
77.8%; Pred. No. 0.00024;
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    A; Reference number: JC2471; MUID:95126979
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                                                                             A; Molecule type: protein
A; Residues: 1-1409 < UVA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 14; Conserv
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A. Residues: 1-1429 COGU>
A. Forosa: references: GB:D14552; NID:g397828; PIDN:BAA03415.1; PID:g408806
C. Function:
A. Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C. Superfamily: GLGF domain homology; Ravodoxin homology; NADPH--ferrihemoprotein; F:23-95/Domain: GLGF domain homology CGG>
F:725-745/Region: calmodulin binding *status predicted
F:755-1394/Domain: NADPH--ferrihemoprotein reductase homology <FEH>
F:755-1394/Domain: NADPH--ferrihemoprotein reductase homology <FEH>
F:757-935/Domain: Ravodoxin homology <FLX>
F:881-912/Region: FMN binding *status predicted
F:1245-1263,1343-1358/Region: NADP binding *status predicted
F:374/Binding site: phosphate (Ser) (covalent) *status predicted
F:415/Binding site: heme iron (Cys) (axial ligand) *status predicted
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A; Accession: $25812
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: 99-112;122-130;132-142;305-318;361-369;457-464;474-480;670-677;734-738;821-8
B; Uvarcov, V.Y.: Lyashenko, A.A.
Biochem. Biophys. Res. Commun. 206, 736-741, 1995
A; Title: The identification of the pterin-binding domain in the nitric oxide synthase's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Species: 37:Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: JN0609
R;Ogura, T.; Yokoyama, T.; Fujisawa, H.; Kurashima, Y.; Esumi, H.
Bjochem. Biophys. Res. Comnun. 193, 1014-1022, 1993
A;Title: Structural diversity of neuronal nitric oxide synthase mRNA in the nervous systAxeference number: JN0609; MUID:93312283
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C;Date: 22-dan-1993 #text_change 04-Mar-2000
C;Date: 22-dan-1993 #sequence_revision 22-34
C;Accession: S16233; S25812; JC2471; PC2184
R;Bredt, D.S.; Hwang, P.M.; Glatt, C.E.; Lowenstein, C.; Reed, R.R.; Snyder, S.H.
Nature 351, 714-718, 1991
Nature: 1991
A;Title: Cloned and expressed nitric oxide synthase structurally resembles cytochrome A;Reference number: S16233; MUID:91287795
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron;
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                                                                                                                                                       Length 136;
                                                                                                                                                   Score 79; DB 2; Length 136 Pred. No. 1.4e-05; 3; Mismatches 0; Indels
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Pred. No. 0.00024;
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A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-1429 <BRE1>
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A;Status: nucleic acid sequence not shown
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Best Local Similarity 80.0°
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Best Local Similarity 77.8
Matches 14; Conservative
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Length 1429;

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C;Keywords: chromoprotein; flavoprotein; heme; iron; metalloprotein; oxidoreductase F;23-95/Domain: GLGF domain homology <GLGS F;75-1398/Domain: NADPH--ferihemoprotein reductase homology <FEH> F;75-139/Domain: NADPH--ferihemoprotein reductase homology <FEH> F;761-939/Domain: flavodoxin homology <FLXx> F;761-939/Domain: flavodoxin homology <FLXx
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; 0 0; Gaps Ouery Match 75.7%; Score 78; DB 2; Length 1433; Best Local Similarity 77.8%; Pred. No. 0.00024; Matches 14; Conservative 0; Mismatches 4; Indels

1 GIVPFRSFWQORLHDSOH 18 || || || || || || || 1 |156 GIAPFRSFWQORQFDIQH 1273

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Search completed: September 10, 2001, 14:01:13 Job time: 212 sec

Sequence 10, Appl Sequence 6, Appl Sequence 9, Appl Sequence 23, Appl Sequence 2, Appl Sequ

Sequence 13,

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GENERAL INFORMATION:
APPLICANT: Billiar, Timothy R.
APPLICANT: Nussler, Andreas K.
APPLICANT: Geller, David A.
APPLICANT: Simmons, Richard L.
APPLICANT: CDNA Clone for Human Inducible Nitric
TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: PA
COUNTRY: USA
ZIP: 15219
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,917
US-08-319-866-10
US-09-123-708-6
US-08-123-708-6
US-08-123-624-6
US-08-047-026A-23
US-08-047-026A-23
US-08-053-703A-2
US-08-06-021-2
US-08-053-703A-3
US-08-553-703A-3
US-08-553-703A-3
US-08-553-703A-2
US-08-553-279-2
US-09-28-523-2
US-09-28-6-23-2
US-08-924-847A-2
US-08-924-847A-2
US-08-922-13
PCT-US95-08565-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Arnold B. Silverman
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 600 Grant Street, 42nd Floor
CITY: Pittsburgh
                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/981,344
FILING DATE: 25-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116972
                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/08314917
; Patent No. 5468630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Silverman, Arnold B.
REGISTRATION NUMBER: 22,614
REFRENCE/CDCKET NUMBER: 1169
TELECOMMUNICATION INFORMATION:
TELEPHONE: (412) 566-6000
MINISTRAESAX: (412) 566-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 866172
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1153 amino acids
   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-314-917-2
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   TOPOLOGY:
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     Query Match
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     Sequence 2, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 2, Appli
                                                                                                                  ; Search time 35.97 Seconds (without alignments) 10.304 Million cell updates/sec
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Sequence 13, Ap
Sequence 11, Ap
Sequence 11, Ap
Sequence 4, Ap
Sequence 21, Ap
Sequence 4, Ap
Sequence 21, Ap
Sequence 21, Ap
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1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
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5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-255-046-2
US-08-265-046-2
PCT-US93-11401-2
PCT-US93-11401-2
US-08-147-812-5
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US-09-123-624-2
US-09-123-624-2
US-09-123-624-13
US-08-866-11
US-08-866-11
US-08-866-11
US-08-866-11
US-09-010-998-5
US-09-010-998-5
US-09-220-574-4
US-09-123-748-4
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US-08-365-486A-19
US-08-880-342-19
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US-07-908-245-2
                                                                                                                                                                                                                                                                                                          197339 seqs, 20590346 residues
                                                                                                                       September 10, 2001, 13:58:11
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                          Scoring table:
                                                                                     OM protein
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Maximum DB
                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                       Run on:
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Result No.

Length 1153;

DB 1;

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PCT-US93-11401-2

Sequence 2, Application PCTUS9311401

Sequence 2, Application PCTUS9311401

GENERAL INFORMATION:

APPLICANT: Billiar, Timothy R.

APPLICANT: OGiler, David A.

APPLICANT: Simmons, Richard L.

TITLE OF INVENTION: CDNA Clone for Human Inducible Nitric

TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
  CDNA Clone for Human Inducible Nitric
Oxide Synthase And Process for Preparing Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1153;
                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: CAPPLICATION NUMBER: PCT/US93/11401 FILING DATE: 25-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 103; DB 2; 100.0%; Pred. No. 4.8e-09; ttive 0; Mismatches 0;
TITLE OF INVENTION: CDNA Clone for Human Indu WIMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ARBESSE: Lewis F. Gould, Jr. ADDRESSEE: Lewis F. Gould, Jr. ADDRESSEE: Eckert Seamans Cherin & Mellott STREET: 1700 Market St. Suite 3232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Arnold B. Silverman
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 600 Grant Street, 42nd Floor
CITY: PLITSburgh
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: GOULD, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REPERENCE/DOCKET NUMBER: 116972-6
TELEPGOMUNICATION INFORMATION:
TELEPHONE: (215) 575-6020
TELEFAX: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   985 GIVPFRSFWQQRLHDSQH 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2. SEQUENCE CHARACTERISTICS: LENGTH: 1153 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GIVPFRSFWQORLHDSQH 18
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                                                                                                                                                                                                                         ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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ZIP: 15219
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                         USA
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                                                                                                                                                                                    STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-465-522-2
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                         Indels
                                                                                                                                                                                                                                                                                                             APPLICANT: Edith Tzeng
APPLICANT: Andreas K. Nussler
APPLICANT: Andreas K. Nussler
APPLICANT: David A. Geller
APPLICANT: Baid A. Geller
APPLICANT: Brichard L. Simmons
TITLE OF INVENTION: Inducible Nitric Oxide Synthase
TITLE OF INVENTION: Gene for Treatment of Disease
NUMBER OF SEQUENCES: 2
CORRESPONDERSEE: Lewis F. Gould, Jr.
ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 1700 Market Street, Suite 3232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION: US/08/265,046
FILING DATE: 24-JUN-1994
CLASSIFICATION: 536
  100.0%; Pred. No. 4.8e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 103; DB 1;
100.0%; Pred. No. 4.8e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Gould, Lewis F. Jr.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 119130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08465522;
Patent No. 5882908
GENERAL INFORMATION:
APPLICANT: Billiar, Timothy R.
APPLICANT: Geller, David A.
APPLICANT: Simmons, Richard L.
                                                                                                                                                                                                                            Sequence 2, Application US/08265046
Patent No. 5658565
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             APPLICANT: Timothy R. Billiar
                                                                                            985 GIVPFRSFWQQRLHDSQH 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       985 GIVPERSFWQQRLHDSQH 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                     1 GIVPFRSFWQQRLHDSQH 18
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Best Local Similarity 100.
Matches 18; Conservative
  Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-265-046-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                  RESULT 2
US-08-265-046-2
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US-08-465-522-2
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Length 1153;

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100.0%; Score 103; DB 5;
100.0%; Pred. No. 4.8e-09;
tive 0; Mismatches 0;
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Matches 17; Conservative
                                           Conservative
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CITY: Rahway
STATE: New Jersey
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3Y: linear
     Query Match
Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY:
US-08-147-812-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-08-319-866-12
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US-08-147-812-5
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                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Length 1153;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07849
                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 103; DB 5;
100.0%; Pred. No. 4.8e-09;
trive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Eckert Seamans Cherin & Mellott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Eckert Seamans Cherin & Mel.
STREET: 1700 Market Street, Suite 3232
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119130-2
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/981,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-07849-2; Sequence 2, Application PC/TUS9507849; GENERAL INFORMATION:
                                                                                                                              116972
                                               ATTORNEY/AGENT INFORMATION:
NAME: SILVETMEN, ATROID B.
REGISTRATION NUMBER: 22,614
REFERENCE/POCKET NUMBER: 11697
TELECOMMUNICATION INFORMATION:
TELEPHONE: (412) 566-6099
TELEX: 866172
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Gould, Lewis F. Jr.
REGISTRATION NUMBER: 25,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION: (215) 575-6020
TELEFAX: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                985 GIVPFRSFWOORLHDSQH 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GIVPFRSFWQQRLHDSQH 18
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11401-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
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                                                                             APPLICANT: Xie, Qiao-wen
APPLICANT: Nathan, Carl F.
APPLICANT: Mathan, Carl R.
APPLICANT: Mumford, Richard A.
APPLICANT: Calaycay, Jimmy Ramos
APPLICANT: Calaycay, Jimmy Ramos
APPLICANT: Calaycay, Jimmy Ramos
CONTRESPONDENCES: 6
CORRESPONDENCE: 6
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08319866
; Patent No. 592923
GENERAL INFORMATION:
APPLICANT: Tully, Timothy P.
APPLICANT: Yin, Jerry C.
APPLICANT: Regulski, Michael
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintcsh Centris650
COMPUTER: Macintcsh Centris650
CORTUMARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: No. 576699 Available
CLASSIFICATION 1435
FILING DATE: No. 576699 Available
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/841,641
FILING DATE: 02-FEB-1992
ATTONNEY,AGENT INFORMATION:
NAME: WALLEN, JOHN W III
REGISTRATION NUMBER: 35,403
                                                                                                                                                                                                                                                                     1: Merck & Co., Inc.
126 East Lincoln Avenue
Sequence 5, Application US/08147812
Patent No. 5766909
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 1865.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELERAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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us-08-833-506c-25.rai

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96.1%; Score 99; DB 4; Length 1144;
Query Match
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                                                                                                                                                                                                                                                                                     APPLICANT: SCHRADER, Jurgen
APPLICANT: SCHRADER, Jurgen
APPLICANT: SCHRADER, Jurgen
APPLICANT: GODECKE, Axel
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
CURRENCE: 511169-2004
CURRENT APPLICATION NUMBER: 08/553,503
PRIOR FILING DATE: 1996-03-01
PRIOR FILING DATE: 1996-03-01
PRIOR FILING DATE: 1994-03-31
NUMBER: OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2.1
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                                           Gaps
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APPLICANT: Thippen, Anice
APPLICANT: Hohmeier, Hans-Ewald
APPLICANT: Newgard, Christopher B.
APPLICANT: Newgard, Christopher B.
APPLICANT: Shimabukuro, Michio
APPLICANT: Chen, Guaxun
APPLICANT: Rhodes, Christopher J.
APPLICANT: Rhodes, Christopher J.
APPLICANT: Cousin, Sharon
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO NO-MEDIATED CYTOTOXICITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold """
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 99; DB 4; Length 114-Pred, No. 2.2e-08;
94.4%; Pred. No. 2.2e-08; ... wismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                 ; Sequence 2, Application US/09123624
; Patent No. 6149936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 96.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                     979 GIAPFRSFWQQRLHDSQH 996
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                 Best Local Similarity 94.48
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Mus musculus
US-09-123-624-2
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-126-109-12
                                                                                                                                                                                                           US-09-123-624-2
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APPLICANT: SCHRADER, JUERGEN
APPLICANT: SCHRADER, JUERGEN
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
FILE REFERENCE: 511169-2003
CURRENT APPLICATION NUMBER: U8/09/123,708
CURRENT FILING DATE: 1998-07-28
EARLIER FILING DATE: 1996-03-31
EARLIER FILING DATE: 1996-03-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VOF: 2.0
SEQ ID NO 2.
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                     TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
                                                                                                                                                                             COMPUTER READABLE FORM:

ZIP: 02133

COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/319,866
FILING DATE: 7-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                         NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.1%; Score 99; DB 2; I 94.4%; Pred. No. 2.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSHL94-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  979 GIAPFRSFWQQRLHDSQH 996
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GIVPFRSFWQQRLHDSQH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 96.1
Best Local Similarity 94.4
Matches 17; Conservative
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; ORGANISM: Cytomegalovirus
US-09-123-708-2
                                                                                                                         CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
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US-08-365-486A-13
Sequence 13, Application US/08365486A
Sequence 13, Application US/08365486A
Sequence 13, Application US/08365486A
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Canbridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1429;
                                                                                                  75.7%; Score 78; DB 1; Length 1429; 77.8%; Pred. No. 8.3e-05;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/365,486A
FILING DATE: 23-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 78; DB 2; I
Pred. No. 8.3e-05;
0; Mismatches 4;
                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08319866; Patent No. 592923; GENERAL INFORMATION: APPLICANT: Tully, Timothy P. RAPLICANT: Rin, Jerry C. APPLICANT: Regulski, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Sholtz. Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-
TELECOMMUNICATION INFORMATION:
TELEFORE: (415) 324-0860
INFORMATION FOR SEO ID NO: 13:
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77.8%;
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1252 GIAPFRSFWQQRQFDIQH 1269
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                                                                                                  Query Match
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-642-002-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-365-486A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-08-319-866-11
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APPLICANT: Bredt, David S.
APPLICANT: Hwang, Paul M.
APPLICANT: Hwang, Paul M.
APPLICANT: Redf, Randall
APPLICANT: Redf, Randall
APPLICANT: Snyder, Solomon H.
TITLE OF INVENTION: Purification and Molecular Cloning of Nitric
TITLE OF INVENTION: Oxide Synthase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 99; DB 4; Length 1146;
Pred. No. 2.2e-08;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...urkSSEE: Banner, Birch, McKie & Beckett
STREET: One Thomas Circle, NW
CITY: Washington
STATE: DC
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,092
FILING DATE: 30-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US UNKNOWN
FILING DATE: 03-MAR-1998
ATONNEY/AGENT INFORMATION:
NAME: MCALLILIAN, Nabeela R.
REGISTRATION NUMBER: P-43.363
RECISTRATION NUMBER: UTSD:560
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1146 anino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,002
FILING DATE: 19910118
CLASSIFICATION: 435
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ATTORREY/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 296-5500
TELEFAX: (202) 296-7830
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/07642002
Patent No. 5268465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.18;
94.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.4'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-126-109-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMINO ACID
                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-642-002-2
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Score 78; DB 4; Length 1429;
Pred. No. 8.3e-05;
0; Mismatches 4; Indels
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Patent No. 5908756
GENERAL INFORMATION:
APPLICANT: STATE Samie R.
TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric CONTRESPONDENCES: 16
NUMBER OF SEQUENCES: 16
CONTRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,625
FILING DATE: 30-AUG-1996
CLASSIFICATION: 530
                                                                                                                           FILING WALE: 43-10W-1337,
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
SEQUENCE CHARACTERISTICS:
LENGTH: 1429 amino acids
23-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: KAGAD, SATAD A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELEFRONE: 202-508-9100
TELEFRAX: 202-508-9100
INFORMATION FOR SEQ ID NO: 4:
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Best Local Similarity 77.8%;
Matches 14; Conservative
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                          CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-880-342-13
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-08-705-625-4
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is Sequence 13, Application US/08880342

is Patent No. 6218179

is Patent No. 6218179

is GENERAL INFORMATION:

APPLICANT: Webster, Keith A.

APPLICANT: Bishopric, Namette H.

APPLICANT: Bishopric, Namette H.

APPLICANT: Green, Christopher J.

TITLE OF INVENTION: Tissue Specific Hypoxia Regulated

TITLE OF INVENTION: Therapeutic Constructs

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: OF U
    TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STARET: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.7%; Score 78; DB 2; Length 1429; 77.8%; Pred. No. 8.3e-05;
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MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/319,866

FILING DATE: 7-OCT-1994

PLOGR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
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NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-5240
INFORMATION (617) 861-540
INFORMATION OF SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1429 amino acids
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Best Local Similarity 77.8
Matches 14; Conservative
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Gaps

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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO Sapiens
US-08-705-625-4
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Search completed: September 10, 2001, 14:01:55 Job time: 224 sec

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AAW81189
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                   Compugen Ltd
                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
        GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                           412676 segs, 60623988 residues
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Maximum Match 100%
Listing first 45 summaries
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AAW81187
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tive 0; Mismatches 0;
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                                                                                       Example 4; Page 37; 93pp; English.
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tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide fragment from human iNOS which is used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autolmmune disease; multiple sclerosis.
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100.0%; Pred. No. 4e-10;
iive 0; Mismatches (
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Pred. No. 4e-10;
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This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                       monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis; Mab.
                                                                                                                                                 nitric oxide synthase; iNOS; human; immunoassay; detection;
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                                                                                      Human iNOS peptide fragment capable of binding Mab 2A12-A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 4e-10;
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                              30-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WEBB/) WEBBER
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                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                    Inducible;
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AAR55764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis; Mab.
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human iNOS peptide fragment capable of binding Mab 1E8-B8.
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Pred. No. 4e-10;
Mismatches 0;
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
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                                                             GIVPFRSFWQQRLHDSQH 18
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Conservative
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18;
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AAW81203 RESULT

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Nucleic acid delivery vehicle comprising a nucleic acid encoding nitric oxide synthase, used for isolated tissue perfusion treatment to enhance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a human inducible nitric oxide synthase (NOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene therapy; angiogenesis; nucleic acid delivery; arteriosclerosis; nitric oxide synthase; NOS; endothelial dysfunction.
                                 An inducible nitric oxide syntase (iNOS or AAR88464) is the product of a cDNA clone (AAT10115) derived from human hepatocytes induced for iNOS biosynthesis. The iNOS can be obtd. by expression of the CDNA e.g. in mammallan host cells and is used in the development of selective inhibitors of NOS or to treat diseases
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1larity 100.0%; Pred. No. 2.7e-08;
Conservative 0; Mismatches 0;
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Disclosure; Page 54-58; 91pp; English.
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99US-0143101.
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                                                                                                                            affected by nitric oxide
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                                                                                                                                                              1153 AA;
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                       AAQ66914 is from human hepatocyte inducible nitric oxide synthase cDNA clone pHINOS from lambda Zap II cDNA library. The original source was induced human hepatocyte RNA. HINOS cDNA plasmid is pref. transformed in E. coll SOLK (ATCC 69126). The inventors claim a clone with the CDNA sequence in AAQ66914 and a cDNA clone which encodes AAR55764. The cloning and expression of a human tissue nitric oxide synthase cDNA provides a source of the enzyme for therapeutic purposes, for example to prevent the hypotensive shock seen with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                    cDNA clone encoding human inducible nitric oxide synthase - used to prevent the hypotensive shock seen with sepsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inducible nitric oxide synthase; iNOS; hepatocyte; gene therapy; vascular occlusive disease; cancer; infection.
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                                                                                                                                               RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 103; DB 15;
Pred. No. 2.7e-08;
Mismatches 0;
                                                                                                                                             Simmons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatocyte inducible nitric oxide synthase.
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100.0%;
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                                                                                                         (UYPI-) UNIV PITTSBURGH
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N-PSDB; AAT10115.
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les 18; Conserv
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                                 23-NOV-1993;
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                                                                     25-NOV-1992;
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                                                                                                                                         Billiar TR,
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09-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Best Local S
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specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inducible nitric oxide synthase; iNOS; rat; immunoassay; detection; monoctional antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                             This invention describes an immunoassay method where a sample with a
                                                                                                                                                                                                                                                                                 Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 99; DB 19; Length 18 pred. No. 1.8e-09; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat iNOS (982-998) peptide fragment.
                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 21; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW81188 standard; peptide; 18 AA.
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Local Similarity 94.4%;
les 17; Conservative
                                                                                                                                           97US-6667777.
                                                                                                        97WO-US06500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WEBB/) WEBBER
                                                                                                                                                                              (WEBB/) WEBBER
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                                   WO9845710-A1
                                                                                                        11-APR-1997;
                                                                                                                                           07-APR-1997;
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   Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inducible nitric oxide synthase; iNOS; murine; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of a nucleic acid delivery vehicle comprising a nucleic acid encoding nitric oxide synthase, especially useful in gene therapy for enhancing and/or inducing angiogenesis and treating atherosclerosis \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to use of a nucleic acid delivery vehicle comprising a nucleic acid encoding nitric oxide synthase (NOS) activity for the manufacture of a composition for essentially isolated tissue perfusion treatment to enhance and/or induce anglogenesis. The nucleic acid delivery vehicle is particularly useful in gene therapy for the treatment of atherosclerosis.
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                                                                                                                                                                                                                                                                    Nitric oxide synthase; NOS; angiogenesis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 103; DB 22;
Pred. No. 2.7e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse iNOS (978-995) peptide fragment.
                                                                                                                                                                                                                                  Human inducible nitric oxide synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Examples; Page 14-18; 39pp; English.
                                                                                                                      AAB66724 standard; protein; 1153 AA.
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Verlinden S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INTR-) INTROGENE BV.
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                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                            AAB66724;
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AAW81187 RESULT

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979 giapfrsfwqqrlhdsqh 996
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                                                                                                                                                                                                                                                                                                                CDNA library; isoform
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                                                                1144 AA;
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                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                           12-AUG-1998
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Best Local S
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AAW51246
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                                                                                                                 specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inducible nitrogen monoxide synthase (iNOS) was isolated from mice, ar
is encoded by AAQ94252. INOS is homodimer with a mol. wt. of 130 kDA
per subunit. The activity of INOS is independent of calmodulin and
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                        invention describes an immunoassay method where a sample with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotic expression vector for nitrogen-mon:oxide synthase gene useful in the treatment and prevention of diseases of blood vessels
                                            an
binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nitrogen monoxide synthase; inducible; treatment; prevention;
                                         Detection of human inducible nitric oxide synthase - using immunoassay in which a sample is contacted with a specific entity reactive with human iNOS or mimics.
                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                    Score 99; DB 19; Length 18
Pred. No. 1.8e-09;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inducible nitrogen monoxide synthase.
                                                                                                                                                                                                                                                                                                                                                                                     AAR77360 standard; Protein; 1144 AA.
                                                                                   Disclosure; Page 21; 93pp; English
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                                                                                                                                                                                                                                                                    96.18;
94.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                          Conservative
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                     WPI; 1998-594495/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SCHR/) SCHRADER J.
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vascular disease;
                                                                                                                                                                                                                   the invention.
                                                                                                                                                                                                                                      18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by gene therapy
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 Webber R;
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cellular calcium levels. Vectors contg. the DNA are used in the treatment or prevention of vascular diseases, high blood pressure, arteriosclerosis, stenosis or restenosis of blood vessels, esp. coronary vessels after percutane transluminal coronary angioplasty. See AAR77363 and AAR77362 for endothelial and brain-derived NOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to two DNA molecules encoding inducible nitric oxide synthase (iNOS) proteins, where the DNA molecules comprise defined sequences of 4041 and 4165 base pairs given in the specification and the proteins have 1144 amino acids. Also claimed are expression vectors containing the DNA molecules, and recombinant host cells containing the vectors. The DNA molecules are useful for producing the recombinant proteins. The present sequence represents inducible nitric oxide, long
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding inducible nitric oxide synthase proteins – useful for producing recombinant proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inducible nitric oxide synthase, long isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xie O;
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94.4%;
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92US-0841641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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AAW02571
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell;
fatty acid; lipotoxic; cytotoxic; cytokine; osteoporosis;
inflammatory disease; autoimmune disease; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibition of cytokine mediated immunotoxicity of cells can be
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Pred. No. 1.2e-07;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manganese containing superoxide dismutase; MnSOD; IDDM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee Y, Newgard CB;
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, Thigpen A,
                                                                                                                                   AAW96322 standard; Protein; 1146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Inducible nitric oxide synthase.
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(TEXA ) UNIV TEXAS SYSTEM.
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Shimabukurom,
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N-PSDB; AAX08434.
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Ohneda M,
                                                                                                                                                                                                                                            AAW96322;
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synthase (iNOS) (AAM02571) was deduced from conn clones (see also AAT32655) obtd. from rat penile smooth muscle cells (PSMC). 6 Amino acid differences were found from vascular iNOS sequences. Recombinant iNOS or iNOS-expressing transformed PSMC cells can be used to ameliorate erectile vasculogenic dysfunction in the penis for the treatment of impotence (NO is the main mediator of erection). The transformed cells can be implanted directly into corpora cavernosa or retained in microcapsules, pellets, etc., allowing in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating erectile dysfunction by increasing level of nitric oxide synthase - in penile tissue, e.g. by admin. of cDNA or enzyme inducers, also new DNA, vectors, transformed cells and enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The amino acid sequence (AAW02571) of rat inducible nitric oxide
                                                                                                                                                                                                                                                                                                                                                                                                                vascular iNOS, amino acid 1084 is Ile
                                                                                                                                                                                                                      'note= "in vascular iNOS, amino acid 270 is Pro"
                                                                                                                                                                                                                                                                                              /note= "in vascular iNOS, amino acid 591 is Val"
                                                                                                                                                                                                                                                                                                                                                                     "in vascular iNOS, amino acid 741 is Pro or Leu"
                                                                                                                                                                                                                                                  "in vascular iNOS, amino acid 349 is Ala
or Val"
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                                                                                                                 Inducible nitric oxide synthase; iNOS; erectile dysfunction; gene therapy; penile smooth muscle cell; PSMC; impotence.
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                                                                                                                                                                                                                                                                                                                          "in vascular iNOS, amino acid 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 29; Page 37-38; 68pp; English.
                                                                                     Rat inducible nitric oxide synthase.
AAW02571 standard; Protein; 1147 AA.
                                                                                                                                                                                         Location/Qualifiers
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N-PSDB; AAT32655.
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                                                          23-OCT-1996
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                                                                                                                                                              Rattus sp.
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Gaps

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96.1%; 94.4%;

Query Match 96.1 Best Local Similarity 94.4 Matches 17; Conservative

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1 GIVPFRSFWQQRLHDSQH 18

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Search completed: September 10, 2001, 14:00:24 Job time: 168 sec

09k9c2 bacillus ha 09r0w4 rattus norv 09qw28 rattus sp. 09de41 gallus gall 092kk7 pasterrella

099yys drosophila 01598 homo sapien 09529 homo sapien 09ptv0 campylobact 09ptx1 arabidopsis 0121x1 arabidopsis 01255 asccharomyc 096127 plasmodium 09vrw3 drosophila 09vrw3 drosophila 014025 homo sapien 078391 homo sapien 021164 fusarium ox 021164 fusarium ox 092gz7 arabidopsis

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ALIGNMENTS

Q9X3W6 Q14024 Q9Y2H7

fusarium ox

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097419 drosophila
095x0 drosophila
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095x0 drosophila
095x0 arabidopsis
091r71 arabidopsis
099750 homo sapien
09750 drosophila
097513 homo sapien
097513 homo sapien
097202 accharomyc
09nai3 caenorhabdi
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                                                   ; Search time 72.54 Seconds (without alignments) 32.830 Million cell updates/sec
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries
                                     OM protein - protein search, using sw model
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Q9U5X0
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Q9XDM4
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sp_vertebrate:*
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sp_rodent:*
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sp_human:*
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                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                 Ogawa Y., Nishijima S., Goto M., Ida M.;
Cloning and characterization of a novel splice valiant of human inducible nitric oxide synthase.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB022318; BAA37123.1;
HSSP; P35228; 4NOS.
InterPro; IPR001094; -.
InterPro; IPR001094; -.
InterPro; IPR001709; -.
InterPro; IPR001709; -.
InterPro; IPR003097; -.
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                                                                                                                                                                                                                                                                                                                                   Pfam: PF00175; Oxidored_fad; 1.
Pfam: PF00167; FAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNOR.
SEQUENCE 1114 AA; 126748 MW; CIF9624774435571 CRC64;
                                         Last sequence update)
Last annotation update)
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100.0%; Pred. No. 6.3e-08;
iive 0; Mismatches 0;
PRT; 1114 AA
                             Created)
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PRELIMINARY;
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Best Local Similarity
Matches 18; Conserv
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SEQUENCE FROM N.A.
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RESULT

Q9zsp0 oryza sativ Q9kud0 vibrio chol Q17845 caenorhabdi Q94181 caenorhabdi

Q9LR71 Q99077 Q9Y5E0 Q9Y5E0 Q9Y5H3 Q02932 Q9NAI3 Q61818 Q97276 Q9ZSP0

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MEDLINE-20196006; PubMed=10731132;

MEDLINE-20196006; PubMed=10731132;

MEDLINE-20196006; PubMed=10731132;

MEDLINE-20196006; PubMed=10731132;

MAMARA M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

MA Amanatides P.G., Nortuan J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

MA M.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

MA M.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

MA M.H., Benos P.V., Barran B.P., Bhandari D., Bolshakov S.,

MA Beeson K.Y., Benos P.V., Berman B.P., Broktier P.,

Martis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

MA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

MA Podson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
px OR CG11084.
Drosophila melanogaster (Fruit fly).
Brusaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                         MEDLINE-98431941; PubMed-9746458;
Wang X., McGregor C.G.A., Miller V.M.;
"Induction and cDNA sequence of inducible nitric oxide synthase from canine aortic smooth muscle cells.";
Am. J. Physiol. 275:H1129-H1129(1998).
EMBL; AF077821; AAC78630.1; --
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                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 16, Last annotation update)
101-MAR-2001 (TrEMBLrel. 16, Last annotation update)
101-MAR-2001 (SATHASE.
Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Canis.
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Pfam; PF00667; FAD_binding; 1.
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PRINTS; PR00371; FPNCR.
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InterPro; IPR001094; -.
InterPro; IPR001433; -.
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrlera S., Fleischmann W., Rosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., R. Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harrey D., Helman T.J., Hernandez J.R., Houck J., Radali M., Ralush F., Karpen G.H., Kenlson J.A., Ketchum K.A., Radali M., Ralush F., Karpen G.H., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McDherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., R. Pelazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., R. Reinert K., Remington K.S., Sunders R.D.C., Scheeler F., Shen H., Spier E., Spradling A.C., Stapleton M., Stupski M.P., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Mongole T., Worley K.C., Wu D., Yang S., Yao Q.A., Wang Z.-Y., Wasaarman D.A., Weinstock G.M., Weissenbach J., A., Lang X.H., Wang X.H., Wong F.N., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Sheng X.H., Who R. S., Wyers E.W., Rubin G.M., Venter J.C., Stapleston M., Strupski M.S., Sun E., Sandry X.H., Zhong F.N., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Strupski M.S., Walles R.S., Wyers E.W., Rubin G.M., Venter J.C.; Hardingaster.", Sheng L., Contrant M. Rubin G.M., Venter J.C.; Hardingaster.", Staple Genece Of Drosophila melanogaster.", Staple Genece Of Drosophila melanogaster."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: CONTAINS LIM DOMAIN(S). THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIM-ISOCENIC DP CN BW;
MEDLINE-99415814; PubMed-10485852;
Gubb D., Green C., Huen D., Coulson D., Johnson G., Tree D.,
Collier S., Roote J.;
"The balance between isoforms of the Prickle LIM domain protein is critical for planar polarity in Drosophila imaginal discs.";
Genes Dev. 13:2315-2327(1999).
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LIM motif; Metal-binding; Zinc.
SEQUENCE 1268 AA; 137228 MW; AC4F9615A7C18C9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Last annotation update)
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InterPro; IPR001781; --
Pfam; PF00412; LIM; 2-
PROSITE; PS00478; LIM_DOMAIN_1; 2.
PROSITE; PS50023; LIM_DOMAIN_2; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2; UNKNOWN_1.
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Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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01-MAR-2001 (TrEMBLrel. 16, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
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HSSP; P04006; 11ML.
FlyBase; FBgn0003090; pk.
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292 PLTAGDLQFENLSLRQ 307
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Best Local Similarity
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300 AA;
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 FROM N.A.
                                                                           SEQUENCE FROM N.A.
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                                             typhimurium
                                                                                                                                                            STRAIN=LT2;
                                                                                                                                                                                                         STRAIN-LT2;
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                                                                                    STRAIN-LT2
                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                           Kearney K., Fitzgerald G.F.;

With Complete Sequence of pC1305 from Lactococcus lactis UC317.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF179848; AAF86686.1; -.

InterPro; IPR002104; -.

Hypothetical protein; Plasmid.

EXEQUENCE 196 AA, 22546 MW; E569B00EE3F7D467 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enterica subsp. enterica serovar Typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                         Length 1299;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 22.5 KDA PROTEIN.
Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Plasmid pc1305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 196;
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                 Prodom; PD000094; -; 2.
PROSTIE; PS50023; LIM_DOMAIN_2; 3.
PROSTIE; PS50028; ZINC_FINGER_C2H2; UNKNOWN_1.
SEQUENCE 1299 Aa: 140529 MW; 3D6D3A31717BE7DE CRC64;
                            EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                        Score 44; DB 5;
Pred. No. 55;
3; Mismatches
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                                                                                                                                                                                                                                               196 AA.
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                               PRT;
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                                                                                                                                         45.8%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.8%;
                           Submitted (JAN-2001) to the EmBL; AJ24310; CAB57345.3; FlyBase; FB000003090; pk. InterPro; IPR000822; -InterPro; IPR001781; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PVTQDDLQYHNLSKQQN 18
SEQUENCE FROM N.A.
STRAIN=ISOGENIC DP CN BW;
Gubb D.C.;
                                                                                                                                       Query Match 45.8
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                        |:| |||: |||:|
292 PLTAGDLQFLNLSLRQ 307
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Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                            2 PVTQDDLQYHNLSKQQ 17
                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                         Pfam; PF00412; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-UC317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella.
NCBI_TaxID=90371;
[1]
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                                                                                                                                                                                                                                                                                                                                  Lactococcus
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Bobik T.A., Xu Y., Jeter R.M., Otto K.E., Roth J.R.;
"Propanediol utilization genes (pdu) of Salmonella typhimurium: three genes for the propanediol dehydratase.";
J. Bacteriol. 179:6633-66319-69711997).
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Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,
Shinn P., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bobik T.A., Busch R.J., Havemann G.D., Williams D.S., Aldrich H.C.; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF026270; AAD39022.1; -. InterPro; IPR000888; -. Probom, PD001462; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                        Chen P., Andersson D.I., Roth J.R.; "The control region of the pdu/cob regulon in Salmonella typhimurium.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bobik T.A., Xu Y., Jeter R.M., Otto K.E., Roth J.R.; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
F21B7.14.
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Pred. No. 18;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                             Bacteriol. 176:5474-5482(1994)
STRAIN-LT2;
MEDLINE-94350831; PubMed-8071226;
                                                                                                                                                                                                                                                                     MEDLINE=98012959; PubMed=9352910;
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Best Local Similarity 52.5.
Conservative
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850 AA

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379 SPFTSDNVNLSNVSQQQ 395
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SEQUENCE 850 A
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01-JUN-2000
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Q9Y5E0
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SEQUENCE 447 AA; 51503 MW; 3A266119927B2FEE CRC64;
             SEQUENCE FROM N.A.
Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafil H., Bei B., Chin C., Chol E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nayyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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Conservation of the b mating-type gene complex among bipolar and tetrapolar smut fungi.;
Plant Cell 5:123-136(1992).
EMBL; Z18531; CAST9217.1;
Mendel; 20793; Ustho;3147;20793.
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Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=120017;
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Pred. No. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                    Ecker J.R.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 647 AA; 70800 MW; 6BF38C5F5493026F CRC64;
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MEDLINE-93177212; PubMed-8439742;
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PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ustilago hordei (Smut fungus).
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Best Local Similarity 61.1%;
Matches 11; Conservative
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2001 (TrEMBLrel. 16,
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Drosopila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikhos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Besson K.Y., Benos P.V., Baxendalle J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Bennan B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                       Gaps
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1942 MW; 1F5489040E08FBC6 CRC64;
                                                                                                                                                             PCDH-GAMMA-A10.
Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PROJOCADHERIN GAMMA A10 SHORT FORM PROTEIN.
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 14, Last annotation update)
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52;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SPVTQDD-----LQYHNLSKQQN 18
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Pfam; PF00028; cadherin; 6.
PRINTS; PR00205; CADHERIN.
PROSITE; PS00232; CADHERIN; 5.
SMART; SM00112; CA; 1.
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Best Local Similarity 38.59
Matches 10; Conservative
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"A striking organization of a large family of human neural cadherin-
the cell adhesion genes.";
Cell 97:779-790(1999).
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-:- SIMILARITY: TO THE CAPHERIN FAMILY.
EMBL; ART52319; AAD43713.1; -.
HSSP; P15116; 1NCJ.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 856 AA; 93777 MW; 3B6C3F80DFEA12B7 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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MEDLINE-99308636; PubMed-10380929;
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Pfam; PF00028; cadherin; 6.
PRINTS; PR00205; CADHERIN: PROSITE; PS00232; CADHERIN: 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE003815; AAF58260.1; -. Flybase; FBgn0033922; CG13942.
Interpro: IPR002965; -.
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61.5%;
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Best Local Similarity 61.5°
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MEDLINE-97313271; PubMed-9169875;

MEDLINE-97313271; PubMed-9169875;

MEDLINE-97313271; PubMed-9169875;

MEDLINE-97313271; PubMed-9169875;

MEDLINE-97313271; PubMed-9169875;

A Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E., Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,

A Delius H., DiPaclo T., Dubois E., Dusterhoft A., Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U., Heumann K., Hilbert H., Hillier L., Hunicke-Smith S., Myman R., Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F., Mewes H.W., Mirtipati S., Moestl D., Muller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M., Schafer M., Schafer M., Scherens B., Schramm S., Schrems S., Schremm S., Schrems S., Schremm S., Schrems S., Schre
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MEDLITHS=8504621; PubMed=6094498;
MEDLITHS=8504621; PubMed=6094498;
Sumrada R.A., Cooper T.G.;
"Nucleotide sequence of the Saccharomyces cerevisiae arginase gene
"Nucleotide sequence of the Saccharomyces cerevisiae arginase gene
"CAR1) and its transcription under various physiological conditions.";
J. Bacteriol. 160:1078-1087(1984).
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MEDLINE=90037050; PubMed=2681212;
Anderson M.S., Muchlbacher M., Street I.P., Proffitt J., Poulter C.D.;
"Isopentenyl diphosphate:dimethylallyl diphosphate isomerase. An
improved purification of the enzyme and isolation of the gene from
Saccharomyces cerevisiae.";
SMART; SM00112; CA; 1.
Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Transmembrane.
SEQUENCE 936 AA; 101445 MW; 5F614F1934D5DC61 CRC64;
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"A suppressor of yeast spp81/dedl mutations encodes a very similar
putative ATP-dependent RNA helicase.";
Mol. Microbiol. 5:805-812(1991).
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Zheng Y., Cerione R., Bender A.;
"Control of the yeast bud-site assembly GTPase Cdc42. Catalysis of
guanine nucleotide exchange by Cdc24 and stimulation of GTPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1032 AA
                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                             44.8%; Score 43; 38.5%; Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 264:19169-19175(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 269:2369-2372(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SPVTQDD-----LQYHNLSKQQN 18
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MEDLINE=91312117; Pubmed=1857205;
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 38.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96078271; PubMed-7476016; Inal Y., Suzukl Y., Mataul T., Tohyama M., Wanaka A., Takagi T.; Inal Y., Suzukl Y., Mataul T., Tohyama M., Wanaka A., Takagi T.; "Cloning of a retinoic acid-induced gene, GTI, in the embryonal carcinoma cell line P19: neuron-specific expression in the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 1840 AA; 196040 MW; A02781CBE26FEBCA CRC64;
                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                      PRT; 1840 AA
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brain Res. Mol. Brain Res. 31:1-9(1995).
EMBL; D29801; BAA06184.1; -.
MGD; MGI:103291; Rail.
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Best Local Similarity 53.3
Matches 8; Conservative
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      Conservative
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| 598 DKLRYKNISKQQ 609
                                                             6 DDLQYHNLSKQQ 17
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Matches 10; Conserv
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TISSUE-BRAIN;
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Q61818
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                                                                                   "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI."; Nature 387:0-0(0).
Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Hussey H., Fortin N., Friesen J.D., Storms R.K., Valall J., Ahmed A., Bussey H., Fortin N., Friesen J.D., Storms R.K., Vo D.H., Wang Y., Winnett E.; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jia Y., Cherry J.M.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U43503; AAB68237.1; -
SGD; SO006046; KAP120.
InterPro; IPR001494; -
SEQUENCE 1032 AA; 119621 MW; 493EDA2B43298F10 CRC64;
                                                                                                                                                                          SEQUENCE FROM N.A. Schlenstedt G., Silver P.A.; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Weber L., Byers B.E.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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Pred. No. 64;
4; Mismatches
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MEDLINE-99069613; PubMed-9851916;
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Science 282:2012-2018(1998).
EMBL; AL032634; CAB5418.1; -.
INTERPRO; IPR002965; -.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 1801 AA: 205015 MW;
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01-OCT-2000 (TrEMBLrel. 15, L&
01-MAR-2001 (TrEMBLrel. 16, LE
Y39GBC. B.
FROTEIN.
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66.7%;
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Best Local Similarity 41.2%;
Matches 7; Conservative
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961 PLTAEQLRYHQLCKNND 977
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Best Local Similarity
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Score 43; DB 11; Length 1840;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID⇔36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowns S., Skelton J., Churcher C., Lawson D., Quail M., Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AL034555, CAB38987.1; - CABSSEQUENCE 1281 AA, 157708 MW; D071C4573BE4C7DE CRC64;
                                         4; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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47.6%; Pred. No. 97;
tive 4; Mismatches
                                         Mismatches
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US-08-833-506C-26 96 1 SPVTQDDLQYHNLSKQQN 18 Title: Perfect score: Sequence:

93435 seqs, 34255486 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•	Description		macaca		P34562 caenorhabdi	_	P43011 haemophilus	-	P57316 buchnera ap	rattus no	O60591 homo sapien	P03513 bunyavirus	085298 buchnera ap	P47708 mus musculu	P39081 saccharomyc	P47709 rattus norv		_	048402 bacteriopha	sacch	homo	рошо	Q95242 sus scrofa	P30572 candida alb		-		_	P32677 escherichia	064689 mus musculu	P70326 mus musculu	_	9849 oryct	Q05086 homo sapien
SUMMARIES	ΙD	2A_	NOS2_MACMU	T3MH_HAEIN	YNP9_CAEEL	PANB_PSEFL	YHCS_HAEIN	CAO1_CANTR	MURE_BUCAI	NOS2_RAT	NS2D_HUMAN	NCAP_BUNSH	MURE_BUCAP	RP3A_MOUSE	PC11_YEAST	RP3A_RAT	NOS2_CAVPO	MDR5_DROME	GP48_BPSP1	CLG1_YEAST	ZF37_HUMAN	MYB_HUMAN	PEC1_PIG	CHS2_CANAL	SP23_YEAST	NOS2_CHICK	YG1K_YEAST	TMRB_BACSU	YIJO_ECOLI	CAGD_MOUSE	TBX5_MOUSE	DPO1_LACLC	LPH_RABIT	UE3A_HUMAN
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	Q9wxi6 buchnera ap Q02510 staphylococ							Q12674 saccharomyc
RPOA_SPIMX GLCM_HUMAN	PT1_BUCAI LIP_STAEP	PEC1_BOVIN	YQIG_ECOLI	UE3A_MOUSE	YE9G_SCHPO	TF1A_HUMAN	UBP7_YEAST	ATC8_YEAST
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39.6 39.6	39.6 39.6	39.6	39.6	39.6	39.6	39.6	39.6	39.6
38 38	38	388	38	38	38	38	38	38
34 35	36 37	8 6 8 7	40	41	42	43	44	45

ALIGNMENTS

<u> </u>	RESULT 1 NS2A_HUMAN ID NS2A_HUMAN STANDARD; PRT; 1153 AA.
α, ⊔	AC P35228; Q16692; O60757; Q16263; DT 01-FEB-1994 (Rel28, Created)
	DT 30-MAY-2000 (Rel. 39, Last annotation update) DE NITRIC OXIDE SYNTHASE. INDUCTBLE (EC.1.14.13.39) (NOS. TYPE II)
. ш	(INDUCIBLE NOS) (INOS) (HEPATOCYTE NOS) (HEP-NOS).
	GN : NOS2A OR NOS2.
0	Mammalia; Eutheria; Primates;
0	OX NCBL_TaxID=9606;
Α, μ	KN [1]
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. 12.	
ц	Geller D.A., Lowenstein C.J., Shapiro R.A., Nussler A.K.,
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<u>ш</u> ,	Billiar T.R.;
<u>.</u>	"Molecular cloning and
4 0	KI IIOH HUMMI HEPALOCYTUS. BI DECA NE+1 ACES CA: H C A 00.3401-3405/1003.
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<u>.</u>	RA Charles I.G., Palmer R.M.J., Hickery M.S., Bayliss M.T.,
ш,	Chubb A.P., Hall V.S., Moss D.W., Moncada S.;
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щ, 1	RC TISSUE-Articular chondrocytes;
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LE 1	Maler R., Bilbe G., Rediske J., Lotz M.;
<u>.</u>	
μ,	RT cDNA cloning and analysis of mRNA expression.";
щ	
ш,	
ш.	
ш,	
ш,	MEDLINE=95091827; PubMed=7528017;
.	Park C.S., Pardhasaradhi K., Gianotti C.,
ш.	RT "Human retina expresses both constitutive and inducible isolorms of
_	RT nitric oxide synthase mRNA.";

2

IN MACROPHAGES,

DIVERSE FUNCTIONS THROUGHOUT THE BODY.

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"Structural characterization of nitric oxide synthase isoforms reveals striking active-site conservation.";
Nat. Struct. Biol. 6:233-242(1999).
-i-FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Crystal structures of zinc-free and -bound heme domain of human inducible nitric-oxide synthase. Implications for dimer stability and comparison with endothelial nitric-oxide synthase.";
                                                                                                                                                                      Guo F.H., de Raeve R.H., Rice T.W., Stuehr D.J., Thunnissen F.B.J.M.,
Erzurum S.C.;
                                                                                                                                                                                                "Continuous nitric oxide synthesis by inducible nitric oxide synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 74-504.
MEDIJUNE-99344067; Pubmed-10409685;
Li H., Raman C.S., Glaser C.B., Blasko E., Young T.A., Parkinson J.F.
Whitlow M., Poulos T.L.;
                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Kidney;
MEDLINE-95165725; PubMed-7532248;
MCLay J.S., Chatterjee P., Nicolson A.G., Jardine A.G., McKay N.G.,
Ralston S.H., Grabowski P., Haites N.E., Macleod A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G., Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.; Three members of the nitric oxide synthase II gene family (NOS2A, NOS2B, and NOS2C, colocalize to human chromosome 17."; Genomics 27:526-530(1995).
                                                                                                                                                                                                                                                                                                                                              t
                                    TISSUE-Glioblastoma;
MEDLINE-9515567; PubMed-7531687;
MEDLINE-9515567; PubMed-7531687;
Medrarl A., Zeniya M., Esumi H.;
"Cloning amd functional expression of human inducible nitric oxide synthase (NOS) cDNA from a glioblastoma cell line A-172.";
J. Biochem. 116:575-581(1994).
                                                                                                                                                                                                                                                               TISSUE-Cardiac myocytes;
MEDLINE-97304504; PubMed-9160867;
Luss H., Li R.-K., Shapiro R.A., Tzeng E., McGowan F.X., Yoneyama Hatakayama K., Geller D.A., Mickle D.A.G., Simmons R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE~99173237; PubMed~10074942;
Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,
Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,
Weber P.C.;
                                                                                                                                                                                                                                                                                                                   Billiar T.R.;
"Dedifferentiated human ventricular cardiac myocytes express
inducible nitric oxide synthase mRNA but not protein in response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hawksworth G.M.;
"Nitric oxide production by human proximal tubular cells: a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Taylor B.S., Alarcon L.H., Billiar T.R.; Inducible nitric oxide synthase in the liver: regulation and
                                                                                                                                                                                                            in normal human airway epithelium in vivo.";
Proc. Natl. Acad. Sci. U.S.A. 92:7809-7813(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 82-528
Biochem. Biophys. Res. Commun. 205:85-91(1994).
                                                                                                                                                                                                                                                                                                                                                                       J. Mol. Cell. Cardiol. 29:1153-1165(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 274:21276-21284(1999).
                                                                                                                               SEQUENCE FROM N.A.
TISSUE~Airway epithelium;
MEDLINE~95372368; PubMed~7544004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96047340; PubMed-7558036;
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MEDLINE-98389865; PubMed-9721329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunomodulatory mechanism?";
Kidney Int. 46:1043-1049(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biokhimila 63:766-781(1998).
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                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                     THE ENZYME (BY SIMILARITY).

--- ENZYME REGULATION REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST MITH MOUSE DESCRIPTION INTO THIS ENZYME AND EPECTS MAY BE EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY SIMILARITY).

--- SUBBNIT: HOWODIMER.

--- INSSUE SPECIFICITY: EXPRESSED IN THE LIVER, RETINA, BONE CELLS AND
                                 NITRIC OXIDE + N NADP(+).
COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FWN. ALSO REQUIRES
TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ?AD; FMN; Calcium-binding; Calmodulin-binding;
Zinc; Metal-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS. CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) \circ CITRULLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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MADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                  AIRWAY EPITHELIAL CELLS OF THE LUNG. NOT EXPRESSED IN THE
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                                                                                                                                                                                                                                                                     -!- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES
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Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; NADP; FAD; FMN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L09210; AAA59171.1; --
EMBL; X73029; CAA51512.1; --
EMBL; U05810; AAA5666.1; --
EMBL; U01511; AAA5004.1; --
EMBL; U2525; BAA5531.1; --
EMBL; U2625; BAA5531.1; --
EMBL; U20141; AAB60366.1; --
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Interpro; IPR001433; -.
Interpro; IPR001709; -.
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ZNSI; 07-JAN-00.
4NOS; 04-FEB-00.
163730; -
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EMBL;
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MIM;
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Venter J.C.;
                                       T3MH_HAEIN
P71366;
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              RESULT 3
T3MH_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                              Lane T.E., Buchmeler M.J., Wattry D.D., Fox H.S.;

Expression of inflammatory cytokines and inducible nitric oxide
synthase in brains of SIV-infected rhesus monkeys: applications to
synthase in brains of SIV-infected rhesus monkeys: applications to
HV-induced central nervous system disease.";
Mol. Med. 2:27-37(1996).

I.E. PUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. INOS AND NO MAY
CONTRIBUTE TO SIMIAN IMMUNODEFICIENCY VIRUS (SIV)-INDUCED CENTRAL
CONTRIBUTE TO SIMIAN IMMUNODEFICIENCY VIRUS (SIV)-INDUCED CENTRAL
CONTRIBUTE AND AND FARE.

I.E. CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +
NITRIC OXIDE + N NADP(+).

I.C. -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
THE ENZYME (BY SIMILARITY).

THE ENZYME (BY SIMILARITY)
C. -1- ENZYME REGILATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                             Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
(INDUCIBLE NOS) (INOS) (FRAGMENT).
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 Length 1153;
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Pred. No. 9.4e-07;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
                            Indels
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 Score 96; DB 1; 1 Pred. No. 2.8e-08;
                            Mismatches
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-1- SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                       TISSUE=Microglia;
MEDLINE=97056192; PubMed=8900532;
                                                                                                                                                                                                                                                           Macaca mulatta (Rhesus macaque).
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Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative 0
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88.9%;
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                                                    1 SPVTQDDLQYHNLSKQQN 18
                                                                  Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                  STANDARD;
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SEQUENCE
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NOS2_MACMU
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                                                            01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
PUTATIVE TYPE III RESTRICTION "MODIFICATION SYSTEM HINDVIP ENZYME MOD (EC. 2.1.1.72) (HINDVIP METHYLTRANSFERASE) (M.HINDVIP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-RD / KW20 / ATCC 51907;
MEDIJNE=93350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterpack T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geognagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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InterPro; IPR002941; -.
Pfam; PF010555; NG_N4_Mtase; 1.
PRINTS; PR00506; D21N6MTFRASE.
PRINTS; PR00508; S21N4MTFRASE.
PROSITE; PS00092; NG_MTASE; 1.
Hypothetical protein; Transferase; Methyltransferase; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 269:496-512(1995).
-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA ADENINE -
S-ADENOSYL-L-HOMOCYSTEINE + DNA 6-METHYLAMINOPURINE.
-!- SUBUNT: CONTAINS TWO DIFFERENT SUBUNITS: RES AND MOD. MOD IS
A HOMOTETRAMER (BY SIMILARITY).
-!- SIMILARITY: WITH OTHER TYPE III MOD PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.9%; Score 45; DB 1; Length 629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   629 AA; 71845 MW; 93ADAD909DB41E84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
629 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REBASE; 3701; M.HindORF1056P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U32786; AAC22721.1; -. TIGR; H11056; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002052; -.
                                                                                                                                                                                                                                                                                       Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:||:||:|:
415 DDIQYNNLNKE 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 DDLQYHNLSKQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=727;
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RESULT 4

17 SLVTQDDLQYHSLSKQQN 34

1 SPVTQDDLQYHNLSKQQN 18

g G

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Rainey P.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YHCS_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
YHCS_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P43011;
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                         Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Wilson R., Ainscough R., Anderson K.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Sauders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Sonnhammer E., Staden R.,
Sulston J., Thierry-Wieg J., Thomas K., Vaudin M., Vaughan K.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                          12.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
3-METHYL-2-0XOBUTHOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 1; Length 705; Pred. No. 6.7; 8; Mismatches 2; Indels
                         01-FEB-1994 (Rel. 28, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 80.6 KDA PROTEIN T05G5.9 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Coiled coil.

DOMAIN
15 137 COILED COIL (POTENTIAL).
DOMAIN
160 509 COILED COIL (POTENTIAL).
DOMAIN
1562 641 COILED COIL (POTENTIAL).
SEQUENCE 705 AA; 80637 MW; 9E89873F5FC04966 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 AA.
                                                                                                                                                                   STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.98;
37.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 227079; CAA81596.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S41009; S41009.
WormPep; T05G5.9; CE21153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 ITENDLEVNNMKKEKN 218
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Best Local Similarity 37.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VTQDDLQYHNLSKQQN 18
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  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                 Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000237; -. Pfam; PF01465; GRIP; 1.
                                                                                        Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BRISTOL N2;
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                              Wohldman P.;
                        01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PANB_PSEFL
Q9ZEP8;
YNP9_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                    Durbin R.;
                                                                                                                                                                                                                                                                                                                                                       elegans.";
                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95350630; PubMed-7542800; Patch State St
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                                                                                                                                                                                                                                                                                                                                                                                                                          "Adaptation of Pseudomonas fluorescens to the plant rhizosphere.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: 5,10-METHYLENETETRAHYDROFOLATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-METHYL-2-OXOBUTANOATE - TETRAHYDROFOLATE + 2-DEHYDROPANTOATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chandler M.S., Smith R.A.; "Characterization of the Haemophilus influenzae topA locus: DNA topoisomerase I is required for genetic competence."; Gene 169:28-31(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ130846; CAA10222.1; -.
Transferase; Methyltransferase.
SEQUENCE 266 AA; 27969 MW; 51B59D25C30E03F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CTT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR HI1364 (ORF2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 1;
Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE PANB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-RD / KW20 / ATCC 51907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae.
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59 PVTTDELAYHTAS 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PVTQDDLQYHNLS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                             NCBI_TaxID=294;
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                                                                                                                                                                                                                                                                                                                          STRAIN-SBW25;
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Gaps

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Length 661; Indels

Score 42; DB 1; Pred. No. 20;

43.88;

4; Mismatches Score 42;

99F89CADEE2D3B0A CRC64;

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PIR; B25123; OXCKX5.
InterPro; IPR002655; -:
Pfam; PF01756; ACOX; 1.
Oxidoreductase; Fatty acid metabolism; Peroxisome; Flavoprotein; FAD;
                                                                                                                                                                                            661 AA; 74132 MW;
                                                                                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               2 PVTQDDLQYHNLSKQQ 17
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                             Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MURE OR BU221
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                                                                                                                                                              INIT_MET
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interrio; ....
PREMI. P. 1.
PROSITE: PSO00126; HTH_IS_FAMILY; 1.
PROSITE: PSO0044; HTH_LYSR_FAMILY; 1.
Hypothetical protein; Transcription regulation; DNA-binding.
DNA_BIND 19 38 H-T-H MOTIF (POTENTIAL).
ORR VTGISLNF -> RAFIEFLSGLGLCSEIWENHEDNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ACYL-COENZYME A OXIDASE I (EC 1.3.3.6) (ACYL-COA OXIDASE) (PXP-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
Rd.";
Science 269:496-512(1995).
-1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
REGULATORS. STRONG, TO E.COLI YHCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEF3C22374352980 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.8%; Score 43;
63.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: PEROXISOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 AA; 32422 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U20964; AAC43726.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             U32816; AAC23011.1; -. HI1364; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M12161; AAA34363.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candida tropicalis (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMOOCTAMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000847; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | |||::||
178 PQTPDDLEHHN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PVTQDDLQYHN 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- COFACTOR: FAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAO1_CANTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIGR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchnera sp. APS.";
Nature 407:81-86(2000).
-!- FUNCTION: CELL WALL FORMATION. DIAMINOPIMELIC ACID ADDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL-L-ALANYL-D-GLUTAMATE + MESO-2,6-DIAMINOHEPTANEDIOATE = ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANYL-D-GLUTAMYL-MESO-2,6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (Rel. 40, Last annotation update)
UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE
(EC 6.3.2.13) (UDP-N-ACETYLMURAMYL-TRIPEPTIDE SYNTHETASE) (MESO-DIAMINOPIMELATE-ADDING ENZYME) (UDP-MURNAC-TRIPEPTIDE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=TOKYO 1998;
MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Gonome sequence of the endocellular bacterial symbiont of aphids Buchnera Sp. APS.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding.

NP_BIND 116 122 ATP (POTENTIAL).

SEQUENCE 497 AA; 56982 MW; 2BEOCC808B370FBF CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-i- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                               497 AA
                                                                                                                                                                                                                                                                   Created)
Last sequence update)
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52.9%;
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Matches 9; Conservative
|::| |:||:| |
43 PILKVDASYYNLTKDQ 58
                                                                                                                                                                                               STANDARD:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93221515; PubMed-7682072;
Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
"Hepatocytes and macrophages express an identical cytokine inducible nitric oxide synthase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Geng Y.J., Almquist M., Hansson G.K.; "cDNA cloning and expression of inducible nitric oxide synthase from rat vascular smooth muscle cells." Blochim. Biophys. Acta 1218:421-424(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-AStrocytes;
MEDLINE-94231594; PubMed=7513765;
Galea E., Reis D.J., Feinstein D.L.;
"Cloning and expression of inducible nitric oxide synthase from rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mandrup-Poulsen T., Boel E., Nerup J.; "Confing and expression of cytokine-inducible nitric oxide synthase CDNA from rat islets of Langerhans."; Diabetes 44:753-758(1995).
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Vascular smooth muscle;
MEDLINE-9191721; Pubmed-7680561;
Nunokawa Y., Ishida N., Tanaka S.;
"Cloning of inducible nitric oxide synthase in rat vascular smooth muscle cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94039059; PubMed-7693462;
Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K., Kawasaki H., Sugimura T., Esumi H.;
"Molecular cloning of a cDNA encoding an inducible calmodulin-dependent nitrig-oxide synthase from rat liver and its
                               NGS2_RAT STANDARD; PRT; 1147 AA, 006518; PS7774; 035765; 064558; Q645065; Q63267; O1-UW-1994 (Rel. 29, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-2000 (Rel. 34, Last sequence update) NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II) (INDUCIBLE NOS) (INOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Karlsen A.E., Andersen H.U., Vissing H., Larsen P.M., Fey S.J., Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Kosuga K., Yul Y., Hattori R., Sase K., Eizawa H., Aoyama
Inoue R., Sasayama S.;

"Cloning of an inducible nitric oxide synthase from rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 191:767-774(1993).
                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 191:89-94(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY; TISSUE-Hepatocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-WISTAR; TISSUE-Pancreatic islets; MEDLINE-95309542; PubMed-7540573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN∴SPRAGUE-DAWLEY; TISSUE∴Aorta;
MEDLINE-94325351; PubMed⊶7519448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Neurosci. Res. 37:406-414(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression in COS 1 cells.";
Eur. J. Biochem. 217:37-43(1993).
                                                                                                                                                                                        Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN HINIBITS EXPRESSION AND FUNCTION OF THIS BNIZME AND EFFECTS MAY BE EXERPED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY
                                                                                                                                                                                 SEQUENCE OF 426-788 FROM N.A. STRAIN; TISSUE-Vascular smooth muscle; STRAIN-DARL/RAPP SALT SENSTIIVE STRAIN; TISSUE-Vascular smooth muscle; MPDILINE-98195092; PubMed-9535418; Chen P.Y., Gladish R.D., Sanders P.W.; Chen P.Y., Gladish R.D., Sanders P.W.; "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBGUNT: HOMODIMER (BY SIMILARITY).
-!- TISSUE SPECIFICITY: IN NORMAL KIDNEY, EXPRESSED PRIMARILY IN THE MEDULLARY THICK ASCENDING LIMB, WITH MINOR AMOUNTS IN THE MEDULLARY COLLECTING DUCT AND VASA RECTA BUNDLE.
-!- INDUCTION: BY INTERFERON GAMMA AND LIPOPOLYSACCHARIDE.
-!- SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                  'Sequence analysis of inducible nitric oxide synthase in rat kidney,
                                                                                                                                                                                                                                                                                                                                          STRAIN-WISTAR; TISSUE Renal glomerulus; Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S.; "Advances in the studies of NO synthesis regulation in mesanglial
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=SPRAGUE-DAWLEY; TISSUE~Renal glomerulus;
MEDLINE~94276509; PubMed~7516453;
Morrissey J.J., McCracken R., Kaneto H., Vehaskari M., Montanl D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Location of an inducible nitric oxide synthase mRNA in the normal
                                                              MEDLINE-97070590; Pubmed-8913516;
Tsutsumishita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,
                                                                                                                                    lung, and uterus.";
Biol. Pharm. Bull. 19:1374-1376(1996)
polymorphonuclear neutrophils."; Endothelium 2:217-221(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kidney Int. 45:998-1005(1994).
                                                                                                                                                                                                                                                                         salt-sensitive rats.";
Hypertension 31:918-924(1998).
                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 509-740 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 479-655 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 420-479 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                Nefrologia 16:35-39(1996).
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U03699; AAC13747.1;
D12520; BAA02090.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L12562; AAA41720.1;
EMBL; X76881; CAA54208.1;
                                                                                                    Futaki S., Niwa M.;
                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Myocardium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NITTIC OXIDE 2:242-249(1998).

-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS. MAY BE INVOLVED IN THE PATHOGENESIS OF DILATED CARDIOMYOPATHY OR OF EXERCISE INTOLERANCE OBSERVED IN PATIENTS WITH CHRONIC HEART FAILURE.
-!- CATALTIT CATIVITY: L-ARGININE + N NADPH + M O(2) - CITRULLINE + NITRIC OXIDE + N NADPH + M O(2) - CITRULLINE + INTRIC OXIDE + N NADPH + M O(2) - CITRULLINE + INTRIC OXIDE + N NADPH + M O(2) - CITRULLINE + INTRIC OXIDE + N NADPH + M O(2) - CITRULLINE + INTRIC OXIDE + N NADPH + M O(2) - CITRULLINE + INTRIC OXIDE + N NADPH + M O(2) - CITRULLINE + INTRIC OXIDE + N NADPH + M O(2) - CITRULLINE + INTRIC DATE + NADPH + M O(2) - CITRULLINE + NADPH + M O(2) - CITRULLI
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CALMODULIN BINDING (POTENTIAL).

FAM (PYRIMIDINE PART) (BY SIMILARITY).

FAD (ADP PART) (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

NADP (RIBOSE PART) (BY SIMILARITY).

ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
PRINTS; PR00361; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding; Heme; Zinc; Metal-binding; Multigene
30-MAY-2000 (Rel. 39, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
NITRIC OXIDE SYNTHASE, INDUCIBLE IID (EC 1.14.13.39) (NOS, TYPE II (INDUCIBLE NOS).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED IN THE HEART AND SKELETAL MUSCLE
--- TISSUE SPECIFICITY: EXPLIGNE, BUT NOT IN HEALTHY INDIVIDUALS.
-!- SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                     TISSUE-Skeletal muscle, and Heart muscle;
MEDLINE-9906690; PubMed-9851365;
Adams V., Krabbes S., Jiang H., Yu J., Rahmel A., Gielen S.,
Schuler G., Hambrecht R.;
"Complete coding sequence of inducible nitric oxide synthase from human heart and skeletal muscle of patients with chronic heart
                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE ENZYME (BY SIMILARITY).
ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF049656; AAC83553.1; -. EMBL; AF051164; AAC83554.1; -. HSSP; P29477; INOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001094; -. InterPro; IPR001433; -. InterPro; IPR001709; -. InterPro; IPR003097; -.
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775
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                 NCBI_TaxID=9606;
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CALMODULIN BINDING (POTENTIAL).
FAM (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
ZINC (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                             InterPro; IPR001709; -.
InterPro; IPR003097; -.
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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060591; 060604;
30-MAY-2000 (Rel. 39, Created)
                                                        AF006619; AAC16401.1; -. AF006620; AAC16402.1; -.
                                                                                                              U48829; AAB18620.1; -. S71597; AAB31028.2; -. L36063; AAC02242.1; -.
  D44591; BAA07994.1; -. D83661; BAA12035.1; -.
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Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                       InterPro; IPR001094; -. InterPro; IPR001433; -.
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412
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513
515
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HSSP; P29477; INOC.
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RESULT 10

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01-NOV-1997
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P47708;
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SEQUENCE
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RP3A_MOUSE
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1990 (Rel. 39, Last sequence update)
UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE
(EC 6.3.2.13) (UDP-N-ACETYLMURANYL-TRIPEPIDE SYNTHETASE)
                                                                                                                                                                                                                        Viruses; ssRNA negative-strand viruses; Bunyaviridae; Bunyavirus.
NCBI_raxID=11580;
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                                                Length 1147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 1; Length 235;
Pred. No. 8.6;
                                                                  Indels
 > L (IN AAC83554).
> V (IN AAC83554).
FF7E4C7ABA76D820 CRC64;
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                                               Score 41.5; DB 1;
Pred. No. 47;
                                                                                                                                                                  (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 34, Last annotation update)
                                                                                                                                                  235 AA
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                                                                  1; Mismatches
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                                                                                                                                                                                             NUCLEOCAPSID PROTEIN (NUCLEOPROTEIN).
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1076 1076 I - 1129 I - 1147 AA; 130528 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.7%;
50.0%;
                                               43.2%;
55.6%;
                                                                                  1 SPVTQDDLQYHNLSKQQN 18
                                                                                              Query Match
Best Local Similarity 55.69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                Bunyavirus snowshoe hare,
                                                                                                                                                   STANDARD;
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                                                                                                                                                                   21-JUL-1986
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01-OCT-1996
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085298;
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         CONFLICT
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MURE_BUCAP
1D MURE_BL
AC 08529B
DT 15-JUL
DT 30-MAY.
DE UDP-N-1
DE UDP-N-1
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                                                                                                                                                                                                                                     "Sequence analysis of a DNA fragment from Buchnera aphidicola (Aphid endosymbiont) containing the genes dapD-htrA-llvI-ilvH-ftsL-ftsI-murE.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL-L-ALANYL-D-GLUTAMATE + MESO-2,6-DIAMINOHEPPANEDIOATE - ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANXL-D-GLUTAMYL-MESO-2,6-DIAMINOHEPPANEDIOATE.
                                                                                                                                                                                                                                                                                                                                             Curr. Microbiol. 37:214-216(1998).
-!- FUNCTION: CELL WALL FORMATION. DIAMINOPIMELIC ACID ADDING ENZYME
(BY SIMILARITY).
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-!- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED WITH RAS-RELATED PROPEIN RAB-3A IN SYNAPTIC VESICLE TRAFFIC AND/OR SYNAPTIC VESICLE FUSION. COULD PLAY A ROLE IN NEUROTRANSMITTER RELEASE BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID 10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inagaki N., Mizuta M., Seino S.;
"Cloning of a mouse Rabphilin-3A expressed in hormone-secreting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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InterPro; IPR000713; -.
Pfam; PF01225; Mur_l1gase; 1.
Peptidogjycan synthesis; Cell wall; Cell division; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 1; Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-i- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBL_TaxID-98794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 292
292 AA; 33467 MW; A4918644BF300AE8 CRC64;
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(Rel. 35, Last annotation update)
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                                                                                                                                                                             MEDLINE-98353428; PubMed-9688822;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.78;
57.18;
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Matches 8; Conservative
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                                                                                                                                                                                                                   Thao M.L., Baumann P.;
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SEQUENCE FROM N.A.
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626 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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-1- SIMILARITY: TO S.POMBE SPAC4G9.04C AND SOME, TO C.ELEGANS R144.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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MEDLINE=95192063; PubMed=7885847;

Davies C.J., Hutchison C.A. III;

"Insertion site specificity of the transposon Tn3.";

Nucleic Acids Res. 23:507-514(1995).

-!- FUNCTION: COMPONENT OF PRE-MRNA CLEAVAGE AND POLYADENYLATION
FACTOR I, INTERACTS WITH RNA14 AND RNA15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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PROSITE; PS50004; C2_DOMAIN_2; 2.
Repeat; Synapse; Protein transport.
DOMAIN 394 >606 PHOSPHOLIPID BINDING (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 1; Length 606;
Pred. No. 27;
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Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                         TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66634 MW; 29AA79E6A103B192 CRC64;
REGULATING MEMBRANE FLOW IN THE NERVE TERMINAL. SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC11_YEAST STANDARD; PRT; 626 AA. P39081; 004932; 01-FEB-1995 (Rel. 31, Created) 15-JUL-1998 (Rel. 36, Last sequence update) PCF11 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 27;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C2 DOMAIN.
                                                                                                                               -1- SIMILARITY: CONTAINS 2 C2 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCF11 OR YDR228C OR YD9934,13C.
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Similarity 37.5%;
6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 NPVWNETLOYHGITEE 458
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MGD; MGI:102788; Rph3a.
InterPro; 1PR001008; .
InterPro; 1PR001965; .
Pfam; PF00168; C2; 2.
Pfam; PF00628; PHD; 1.
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>606
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STRAIN=S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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SEQUENCE
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AC PC11_Y
AC PC11_Y
AC PC11_Y
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DT 15-UUL
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CN 
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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-!- SUBUNIT: MONOMER.
-!- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN BRAIN.
-!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
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MEDLINE-95033210; PubMed-7946335;
Li C., Takei K., Geppert M., Daniell L., Stenius K., Chapman E.R., Jahn R., de Camilli P., Suedhof T.C.;
Synaptic targeting of rabphilin-3A, a synaptic vesicle
Ca2+/Phospholpid-binding protein, depends on rab3A/3C.";
Neuron 13:885-898(1994).
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"Structural basis of Rab effector specificity: crystal structure a "Structural basis of Rab effector specificity: crystal structure rather small G protein Rab3A complexed with the effector domain of rabphilin 3A.";
cell 96:363-374(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 626;
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NSL -> ILS (IN REF. 2).

I -> V (IN REF. 2).

66F91BA9577E82F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
28;
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41;
Pred. No.
                                                                                                                                                                                                           processing; Nuclear protein.
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MEDLINE=99148269; PubMed=10025402;
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                                                                              EMBL; 248612; CAA88508.1; -. EMBL; U13239; AAC33145.1; -. PIR; S47936; S47936. SGD; S0002636; PCF11.
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Best Local Similarity 46...
7; Conservative
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288
515
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DR InterPro; IPR001965; -.

DR Pfam; PP001068; -2.

DR Pfam; PP001068; -2.

DR Pfam; PP001068; -2.

DR PRINTS; PR00396; C2DOMAIN.

DR PRINTS; PR00399; C2_DOMAIN.

DR PROSITE; PS00049; C2_DOMAIN_2; 2.

KW Repeat; Synapse; Protein transport; 3D-structure.

FT DOMAIN 397 488 C2_DOMAIN.

FT DOMAIN 397 485 C2_DOMAIN.

FT DOMAIN 397 645 C2_DOMAIN.

FT DOMAIN 397 645 C2_DOMAIN.

FT DOMAIN 397 645 C2_DOMAIN.

AS SEQUENCE 684 AA; 75832 MW; 05838BC3C7A86444 CRC64;

Query Match 42.7%; Score 41; DB 1; Length 684;

Best Local Similarity 37.5%; Pred. NO. 31;

Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
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Search completed: September 10, 2001, 14:09:52 Job time: 561 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                      September 10, 2001, 14:01:13
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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C64180
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96
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Maximum DB seq length: 2000000000
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Match Length
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pir2:*
pir3:*
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rabphilin-3A - mou
rabphilin-3A - rat

E81403 S59435 JX0338 I58166

30 41 42.7 991 2 S57385 31 41 42.7 1192 2 A71623 32 41 42.7 1192 2 A71623 33 40 41.7 346 2 S11196 34 40 41.7 346 2 S17607 35 40 41.7 452 2 S77607 36 40 41.7 7 452 2 S77607 37 40 41.7 7 452 2 S77607 38 40 41.7 11082 2 S77837 41 40 41.7 11082 2 S77837 42 40 41.7 11082 2 S77837 43 40 41.7 11082 2 S77837 44 39 40.6 139 2 T43058 45 39 40.6 139 2 T43058 45 39 40.6 139 2 T43058 46 39 40.6 139 2 T43058 47 49 40.6 203 2 T43058 48 40 41.7 1533 2 T43058 48 5 39 40.6 283 2 E65202 48 5 39 40.6 283 2 E65202 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	probable membrane probable secreted multidrug resistan transforming prote probable glycosyla cyclin-like protei two-component sens transforming prote chitin synthase (E suppressor protein hypothetical trans	IGNMENTS	human #text_change 20 6; A47475 3. 3. 47475 of a cDNA encod chassisselve nitr n inducible nitr 2. AAB49041.1; PID 3.7; Thunnissen, cible nitric oxi hown; translatio n articular chon n articular chon hown hown hown hown hown hown hown h	Nussler, A.K.; Di
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30 41 42.7 119 31 41 42.7 119 32 41 42.7 119 33 4 40 41.7 44 34 40 41.7 44 35 40 41.7 44 36 40 41.7 76 37 40 41.7 76 38 40 41.7 76 38 40 41.7 76 39 40.6 115 40 40 41.7 110 40 40 41.7 110 40 40 41.7 110 41.7 76 42 39 40.6 12 43 39 40.6 12 44 39 40.6 12 45 39 40.6 12 47 1110: Cloning, character A.Reference number: A49676; A.Title: Cloning, character A.Reference number: A49676 A.Status: preliminary A.Residues: 1-67, 7609-1 A.Title: Cloning and function A.Residues: 1-607, 71,609-1 A.Residues: 1-607, 71,607-9 A.Residues: 1-607, 71,60	337802588551		nn) 14	υ
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	0.000000000000000000000000000000000000		RESULT A49676 C) Strict C) Date:: C, Date:: C, Acces C, Acces C, Acces A, Resic A, Resic A, Resic A, Resic A, Resic A, Resic A, Acces A, A	R;Gelle Proc. N

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A; Introns: 13/3; 45/2; 68/3; 102/3; 135/3; 286/2; 323/3; 547/3; 565/1; 610/3
                                                                                                                                                                                                  A; Cross-references: EMBL: Z27079; NID:g414641; PID:g414650 C; Genetics:
   to the EMBL Data Library, October 1993 se number: $41001
   submitted to the EMBL Dat.
A;Reference number: $4100
A;Accession: $41009
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-690 <THO>
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A; Residues: 1-288 <TIGR>
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Matches 6; Conserv
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                                                                                                                                                             A. Residues: 1-422, 'I', 424-804,'D', 806-830,'SP', 833-932,'G', 934-965,'A', 967-986,'V', 988-1
A. Cross-references: GB:L09210; NID:g292241; PIDN:AAA59171.1; PID:g292242
A. Cross-references: GB:L09210; NID:g292241; PIDN:AAA59171.1; PID:g292242
A. Note: sequence extracted from NCBI backbone (NCBIP:129733)
C. Genetics:
A. Genetics: GB:NOS2A; NOS2; INOS
A. Cross-references: GDB:139215; OMIM:163730
A. Genetics:
C. Function:
A. Map position: 17cen-17q11.2
C. Function:
A. Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C. Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduce
C. Keywords: calmodulin binding *status predicted
C. Keywords: calmodulin binding *status predicted
F: 509-529/Region: calmodulin binding *status predicted
F: 513-1127/Domain: ilanodoxin homology <FEH>
F: 521-1127/Domain: ilanodoxin homology ckLX.
F: 623-654/Region: FMN binding *status predicted
F: 765-778/Region: FNN binding *status predicted
F: 706-778/Region: PNN binding *status predicted
F: 706-778/Region: NADP-ribose binding *status predicted
F: 707-798-996/Region: NADP-ribose binding *status predicted
F: 700/Relion: NADP-ribose binding *status predicted
F: 1076-1091/Region: NADP-ribose binding *status predicted
F: 200/Relion: Relicion: NADP-ribose binding *status predicted
F: 200/Relion: Relicion: NADP-ribose binding *status predicted
F: 200/Relicion: NADP-ribose binding *status predicted
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C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: 18-ANG-1995 #sequence_revision 18-ANG-1995 #text_change 08-Oct-1999
C;Accession: C64180
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, F.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, J. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weldman, J. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Reference number: A64000; MulD:95350630
A;Reference number: acid sequence not shown; translation not shown
A;Mclecule type: DNA
A;Residues: 1-629 <TIGR>
A;Title: Molecular cloning and expression of inducible nitric oxide synthase from human A;Reference number: A47475; MUID:93234523
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C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C;Accession: S41009
R;Thomas, K.
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                                                                                                          A;Status: preliminary; not compared with conceptual A;Molecule type: mRNA
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100.0%;
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Best Local Similarity 100
Matches 18; Conservative
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Matches 7; Conservative
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415 DDIQYNNLNKE 425
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C; Accession: D64171
R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Googwe, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Woldman, Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Snith, H.O.; Vente A; Reference number: A64000; MUID:95350630
A; Accession: D64171
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A;MoLecule type: DNA
Residucas: 1.447 CSHI>
A;Cross-references: EMBL:AC002560; NID:g2618677; PID:g2809251; GSPDB:GN00059; ATSP:F2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T00906
R;Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; eologis, A.; Ecker, J.R.
submitted to the EMBL Data Library, January 1998
A;Bescription: Genomic sequence for Arabidopsis thaliana BAC F21B7.
A;Reference number: Z14208
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                                                                                                                                                                                                                                                                                                                                hypothetical protein HI1364 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F2187.20 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
                                                                 Gaps
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Length 690;
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Pred. No. 12;
2; Mismatches
Score 45; DB 2;
Pred. No. 15;
8; Mismatches
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46.9%;
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Best Local Similarity 63.6%;
Matches 7; Conservative
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203 ITENDLEVNNMKKEKN 218
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                                                                 6; Conservative
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C;Accession: T30250
R;Imai, Y.; Suzuki, Y.; Matsui, T.; Tohyama, M.; Wanaka, A.; Takagi, T.
Brain Res. Mol. Brain Res. 31, 1-9, 1995
A;Title: Cloning of a retinoic acid-induced gene, GTl,in the embryonal carcinoma cell A;Reference number: 220788; MUID:96078271
A;Accession: T30250
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: CESP:Y39G8C.b
A;Map position: 1
A;Introns: 69/3; 117/2; 186/3; 226/3; 268/3; 371/3; 540/3; 857/1; 881/3; 1025/3; 1077
                                                                                                         Submitted to the EMBL Data Library, October 1998
A; Reference number: 220263
A; Reference number: 220263
A; Accession: T26774
A; Accession: T26774
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1801 < MIL>
A; Cross-references: EMBL:AL032634; PIDN:CAB54418.1; GSPDB:GN00019; CESP:Y39G8C.b
A; Experimental source: clone Y39G8C
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: brain A; Note: expression was specifically localized in neurons but not in glial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 2 [imported] - rice
C;Species: Oryza sativa (rice)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Accession: T51588
R;Sava, S; Watanabe, K; Okada, K.
submitted to the EMBL Data Library, October 1998
A;Reference number: 225399
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T26774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molcoule type: mRNA
A;Residues: 1-1840 < IRAN>
A;Cross-references: EMBL:D29801; NID:g475015; PIDN:BAA06184.1; PID:g475016
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A;Molecule type: mRNA
A;Residues: 1-186 <SAM>A;Residues: 1-186 <SAM>A;Cross-references: BMBL:AF098753; PIDN:AAC72848.1
C;Superfamily: Arabidopsis thaliana hypothetical protein F6N15.22
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Pred. No. 1.1e+02;
3; Mismatches 4
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Pred. No. 11;
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1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 2
Pred. No. 1e+02
2; Mismatches
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Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.3
Matches 8; Conservative
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282 TQETLHYONLAKYQH 296
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598 DKLRYKNISKQQ 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 DDLQYHNLSKQQ 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                      R; Smye, R.
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                                                                                                                                                                                                                                                                                                                                                     Dwest mating protein 2 (UhbW2) - smut fungus (Ustilago hordei)

C; Species: Ustilago hordei (barley smut)
C; Species: Ustilago hordei (barley smut)
C; Species: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 24-Sep-1999
C; Accession: J02149; S33368
R; Bakkeren, G; Kronstad, J.W.
Plant (Cell 5; 123:136, 1993
A; Title: Conservation of the b mating-type gene complex among bipolar and tetrapolar smuth A; Reference number: S3365; MUID:93177212
A; Reference number: S3365; MUID:93177212
A; Residues: 1-647 < BAK>
A; Residues: 1-647 < CBAK>
A; Residues: 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein YPL125w - yeast (Saccharomyces cerevisiae)
Nylternate names: hypothetical protein LPH2w
Nylternate names: hypothetical protein LPH2w
Syspecies: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 05-Nov-1999
C; Accession: S61997
S; Schlomstedt, G.; Silver, P.A.
Submitted to the EMBL Data Library, December 1995
A; Reference number: S61996
A; Reference number: S61996
A; Residues: 1-1032 <SCCH>
A; Molecule type: DNA
A; Residues: 1-1032 <SCCH>
A; Cross-references: EMBL: U43503; NID: 91163087; PID: 91163089; GSPDB: GN00016; MIPS: YPL125w
A; Chonetics:
A; Chonetics: A; Chonetics: A; Chonetics: A; Chonetics: A; Chonetics: A; Chonetics: A; Chonetics: A; Chonetics: A; Chonetics: A; Chonetics: A; Chonetics: A; Chonetics: A; Chonetics: A; Chonetics: Ch
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                                                Indels
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Pred. No. 54;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3
           d. No. 20;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43;
Pred. No.
           Pred.
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   Best Local Similarity 61.1%;
Matches 11; Conservative
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                                                                                                                                                                                    211 VTODDLLYVFSNLSRNVN 228
                                                                                                                3 VTQDDLQY -- HNLSKQQN 18
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Best Local Similarity 47.1*
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Best Local Similarity 41.2.
The 7; Conservative
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B west
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-597 cSTVO>
A;Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06446.1; GSPDB:G
A;Experimental source: strain C-125
A;Genetical Source: strain C-125
A;Genetical Source: strain C-125
A;Genetical Source: strain C-125
A;Genetical Su227
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N;Alternate names: acyl-CoA oxidase I
C;Species: Candida tropicalis
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
C;Accession: B25123
R;Okazaki, K.; Takechi, T.; Kambara, N.; Fukui, S.; Kubota, I.; Kamiryo, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 1232-1236, 1986
A;Title: Two acyl-coenzyme A oxidases in peroxisomes of the yeast Candida tropicalis: A;Reference number: A94084; MUID:86149279
A;Accession: B25123
A;Molecule type: DNA
A;Residues: 1-662 COKA>
A;Cross-references: GB:M12161; NID:g170913; PIDN:AAA34363.1; PID:g170914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      two-component sensor histidine kinase BH2727 [imported] - Bacillus halodurans (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Bacilius halodurans
C;Accession: G83990
C;Accession: G83990
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; I
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans & A;Reference number: A83650; MUID:20263314
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                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-395 <CON>
A;CONS-references: EMBL:U67951; PIDN:AAB07575.1; GSPDB:GN00028; CESP:C47C12.6
A;Experimental source: strain Bristol N2; clone C47C12
hypothetical protein C47C12.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T25651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Introns: 115/3; 148/3; 219/3; 252/3; 274/2; 322/1; 342/3
                                                                                                                                                            Riconnell, M. submitted to the EMBL Data Library, August 1996 A; Description: The sequence of C. elegans cosmid C47C12. A; Reference number: 220062 A; Accession: T25651
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Pred. No. 26;
4; Mismatches
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ced. No. 42;
Mismatches
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Pred. No.
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50.0%;
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Best Local Similarity 50.0
Matches 8; Conservative
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Best Local Similarity 46.7
Matches 7; Conservative
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144 PVTWDELQHHAVTTE 158
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                                                                                                                                                                                                                                                                                                                                                G. Species: Vibrio cholerae
G. Accession: A82304
R. Heidelberg, J. E. Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F. Nature 406, 477-483, 2000
A.Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A. Reference number: A82035; MUID: 20406833
A. Accession: A82304
A. Status: preliminar
A. Molecule type: DNA
A. Residues: 1-264 <HEIS
A. Residues: 1-264 <HEIS
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A. Residues: 1-264 <HEIS
A. Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                               3-methyl-2-oxobutanoate hydroxymethyltransferase VC0592 [imported] - Vibrio cholerae (st
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A; Description: The sequence of C. elegans cosmid C09B8.
A; Reference number: S61138
A; Accession: T15462
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-387 < KTE>
A; Cross references: EMBL:U29612; NID:q868273; PID:g868275; PIDN:AAA68801.1; CESP:C09B8.3
A; Cross references: strain Bristol N2
A; Experimental source: strain Bristol N2
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Date: 20-Sep-1999 #text_change 24-Nov-1999
Accession: T15462
Stellyes, L.
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'Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase
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Pred. No. 25;
3; Mismatches
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16;
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155 TLDNLQYKNLFNERN 169
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C:Comment: This enzyme, located in peroxisomes, catalyzes the oxygen-specific oxidation; this reaction is the initial step of the peroxisomal beta-oxidation system. In C. tropgene family.

C:Comment: The peroxisomes are eukaryote subcellular organelles that generate and degrad ic reactions as well as the enzymes involved are usually different from the mitochondria d:Genetics:

A:Genetics:

A:Genetics:

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ö 0; Gaps Query Match 43.8%; Score 42; DB 1; Length 662; Best Local Similarity 43.8%; Pred. No. 48; Matches 7; Conservative 4; Mismatches 5; Indels |::| |:||:| | 44 PILKVDASYYNLTKDQ 59 2 PVTQDDLQYHNLSKQQ 17 ò

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TYPE: amino acid
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-626-994A-3
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US-08-073-384C-8
US-08-483-043-8
US-08-481-238-8
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US-08-626-994A-3
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US-08-674-030-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
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Appl:	, App	Appl	Appl	Appl	Appl	Appli	5206163	, App.	, App.	, App.	, App	, App.	, App.	, App	, Appl	, App	, Appl
Sequence 8,	Sedneuce 71'	Sequence 2,	Sequence 2,	Sequence 2,	Sequence 1,	Sequence 4,	Patent No. 5	Sequence 50,	Sequence 51	Sequence 50	Sequence 51						
US-08-247-904B-8	US-08-/0/-94.2A-21	US-08-338-530A-2	US-09-267-384-2	US-09-198-956-2	US-08-080-855-1	US-08-713-928B-4	5206163-1	US-08-465-380-50	US-08-465-380-51	US-08-486-397-50	US-08-486-397-51	US-08-486-399-50	US-08-486-399-51	US-08-461-965-50	US-08-461-965-51	US-08-634-641-50	US-09-249-448-51
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38.5	38.5	38	38	38	38	38	37.5	37	37	37	37	37	37	37	37	37	37
8 8	2	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

APPLICANT: Unger, Roger H.
APPLICANT: Shimabukuro, Michio
APPLICANT: Chen, Guaxun.
APPLICANT: Rhodes, Christopher J.
APPLICANT: Hugl, Sigrun R.
APPLICANT: Cousin, Sharon
TITLE OF INVENTION: TO NO-MEDIATED CYTOTOXICITY Thigpen, Anice Hohmeier, Hans-Ewald Newgard, Christopher B. ; Sequence 12, Application US/09126109; Patent No. 6171856 GENERAL INFORMATION:

ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy CITY: Houston STATE: Texas

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,109
FILING APPLICATION SO-JUL-1998
CLASSIFICATION NUMBER: US 60/055,092
FILING BAPLICATION NUMBER: US UNKNOWN
FILING DATE: 30-JUL-1997
PRIOR APPLICATION NUMBER: US UNKNOWN
FILING DATE: 03-MAR-1998
ATTORNEY/AGENT INFORMATION: P-43,363 RRR: UTSD:560 NAME: MOMILIAON, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELECAX: (512) 474-757
INFORMATION FOR SEO ID NO: 12:
SEQUENCE CHARACTERISTICS:

1146 amino acids

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19103
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                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                     Length 1146;
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ZIP: 15219
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IPM PC COMPATIBLE
COMPUTER: PATENTIN RELEASE #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/314,917
                                                                                100.0%; Score 96; DB 4; 1
100.0%; Pred. No. 4.2e-08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 96; DB 1; I
100.0%; Pred. No. 4.2e-08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/981,344
FILING DATE: 25-NOV-1992
AFTORNEY/AGENT INFORMATION:
NAME: $11verman, Arnold B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Silverman, Arnold B.
REGISTRATION NUMBER: 22,614
REPERENCE/DOCKET NUMBER: 1169
TELECOMMUNICATION INFORMATION:
TELEPHONE: (412) 566-6000
TELEFAX: (412) 566-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 866172
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1153 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPVTQDDLQYHNLSKQQN 54
                                                                                                                                        1 SPVTQDDLQYHNLSKQQN 18
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                                                                                Ouery Match
Best Local Similarity 100.
Matches 18; Conservative
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STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-126-109-12
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Best Local Similarity
Matches 18; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                      US-08-314-917-2
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Patent No. 5882908
CENERAL INFORMATION
APPLICANT: Nussler, Andreas K.
APPLICANT: Geller, David A.
APPLICANT: Simmons, Richard L.
TITLE OF INVENTION: ODNA Clone for Human Inducible Nitric
TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                 GENERAL INFORMATION:
APPLICANT: Timothy R. Billiar
APPLICANT: Edith Tzeng
APPLICANT: Andreas K. Nussler
APPLICANT: Andreas K. Nussler
APPLICANT: Pavid A. Geller
APPLICANT: Richard L. Simmons
TITLE OF INVENTION: Inducible Nitric Oxide Synthase
TITLE OF INVENTION: Gene for Treatment of Disease
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,046
FILING DATE: 24-JUN-1994
CLASSIFICATION: 536
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 1700 Market St. Suite 3232
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREER 1700 Market Street, Sulte 3232
CITY: Philadelphia
; Sequence 2, Application US/08265046
; Patent No. 5658565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: GOULD, LEWIS F. Jr.
REGISTRATION NUMBER: 25,057
REFRENCE/DOCKET NUMBER: 1191
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6020
TELEFAX: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SPVTQDDLQYHNLSKQQN 18
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (412) 566-6000
TELEFAX: (412) 566-6099
                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                            ; MOLECULE TYPE: protein PCT-US93-11401-2
                                                                                                                                        amino acid
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Best Local Similarity
Matches 18; Conserva
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Matches 18; Conserv
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APPLICANT: Nussler, Andreas K.
APPLICANT: Geller, David A.
APPLICANT: Simmons, Frohard L.
TITLE OF INVENTION: CDNA Clone for Human Inducible Nitric
TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11401
FILING DATE: 25-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 96; DB 2; I
Pred. No. 4.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Arnold B. Silverman
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREER: 600 Grant Street, 42nd Floor
CITY: Pittsburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: GOULD, Jr., Lewis R.
REGISTRATION NUMBER: 25.057
REFERENCE/DOCKET NUMBER: 116972-6
TELECHONICATION INFORMATION:
TELECHONE: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: PCT/US93/11401
25-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 15219
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/981,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Arnold B.
REGISTRATION NUMBER: 22,614
REFERENCE/DOCKET NUMBER: 116972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application PCTUS9311401 GENERAL INFORMATION:
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
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SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 SPVTQDDLQYHNLSKQQN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SPVTQDDLQYHNLSKQQN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.(
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-465-522-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Pittsburgh
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                        19103
  PA
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RESULT 6
PCT-US95-07849-2
Sequence 2, Application PC/TUS9507849
GENERAL INFORMATION:
APPLICANT: University of Pittsburgh of the Commonwealth System of Higher APPLICANT: Education
TITLE OF INVENTION: Inducible Nitric Oxide Synthase
TITLE OF INVENTION: Gene for Treatment of Disease
NUMBER OF SEQUENCES: 2
CORRESPONDENCE 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 1700 Market Street, Suite 3232
CITY: Philadelphia
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                                                                                                                                                                                                                                                                                       Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07849
                                                                                                                                                                                                                                                                4.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 96; DB 5; ...
nilarity 100.0%; Pred. No. 4.2e-08;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                         100.0%; Score 96; DB 5;
100.0%; Pred. No. 4.2e-08
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLId, LEWIS F. Jr.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 1191
TELECOMMUNICATION INFORMATION:
TELERAX: (412) 566-6099
TELEX: 866172
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (215) 575-6020
TELEFAX: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 1153 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                  1 SPVTQDDLQYHNLSKQQN 18
                                                                                                                                                                                                                                                                                                                                                             37 SPVTQDDLQYHNLSKQQN 54
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Patent No. 5928895
GENERAL INFORMATION:
APPLICANT: Burnham, Martin K.
TITLE OF INVENTION: No. 5928895el IgA Fc Binding Protein NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 3;
Pred. No. 48;
3; Mismatches
                                                                               FILING DATE:
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: UP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
RECISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 716-1180
TELEFAX: (703) 716-1180
TELEFAX: (703) 716-1180
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,030
FILING DATE: 24-5EP-1996
APPLICATION NUMBER: 60/040,656
FILING DATE: 10-MAR-1997
ATTORNEY_AGENT INFORMATION:
NAME: Dickinson, Q. Todd
REGISTRATION NUMBER: 28,354
REFERENCE_COCKET NUMBER: P50545
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215/994-2222
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 40.6%;
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | |::|| || |:
287 PNTREDLPYHYYDKK 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-957-742-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-929-417-2
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48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                 GENERAL INFORMATION:
APPLICANT: Shichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4G1CNAC 2,8-
TITLE OF INVENTION: SIALYLTRANSFERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
CITY: Reston
STATE: Virginia
COUNTY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08957742
Patent No. 6017743
GENERAL INFORMATION:
TITLE OF INVENTION: Sia' 2,3Gala 1,4GICNAC 2,8-
TITLE OF INVENTION: SIA'ZITRANSFERASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PErfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,994A
FILING DATE: APAIJ 3, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 77469/1995
FILING DATE: APAIJ 3, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUDICANTESSEE: Greenblum & Bernstein, STREET: 1941 Roland Clarke Place CITY: Reston STATE: Virginia COUNTY: U.S.A. ZIP: 20191 S.A. COMPUTER READABLE FORM: MEDIUM TYPE: 1.44 diskette COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
TELECOMNUNICATION INFORMATION:
TELEPHONE: (703) 716-1191
TELEFAX: (703) 716-1191
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acid
                                                           Sequence 3, Application US/08626994A Patent No. 5798244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 PNTREDLPYHYYDKK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PVTQDDLQYHNLSKQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-626-994A-3
                                      US-08-626-994A-3
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Gaps

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Sequence 1, Application US/08957742
Patent No. 6017743
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                      CITY: Reston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-073-384C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-957-742-1
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52;
                                                                                                                                                                            DB 2; Length 351;
50;
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4GlCNAC '2,8-
TITLE OF INVENTION: SIA' 2,3Gala 1,4GlCNAC '2,8-
TITLE OF INVENTION: SIALYLTRANSFERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
CITY: Reston
STREET: Virginia
COUNTRY: U.S.A.
21P: 20191
                                                                                                                                                                            Score 39; DB 2
Pred. No. 50;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.6%; Score 39; DB
46.7%; Pred. No. 52;
Live 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word Perfect 5.1+ (ASCII)
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
PRELIGNE DATE: W35
CLASSIFICATION AT 35
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Arnold Turk
REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: 914595
IELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08626994A Patent No. 5798244 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                            40.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (703) 716-1191
TELEFAX: (703) 716-1180
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 amino acids
                                                                                                                                                                            Query Match 40.6
Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 46.7
Matches 7; Conservative
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                                                            TYPE: amino acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PVTQDDLQYHNLSKQ 16
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                                                                                                                                                                                                                                                                              111 DDIQKHHLQKEKH 123
                                                                                                                                                                                                                                                        6 DDLQYHNLSKQQN 18
                                                                                                  ; TOPOLOGY: linear
US-08-929-417-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-626-994A-1
                                                                                                                                                                                                                                                                                                                                                                         US-08-626-994A-1
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US-08-957-742-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Patent No. 5541311

GENERAL INFORMATION:
CENERAL INFORM
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APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia 2,3Gala 1,4G1CNAC '2,8-TITLE OF INVENTION: SIALYLTRANSFERASE
NUMBER OF SEQUENCES: 4
OCRRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.6%; Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word Perfect 5.1+ (ASCII) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,742 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States of America
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Arnold Turk
REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
                                                                                                                                                                                                                                                                                                                                                         STATE: Virginia
COUNTRY: U.S.A.
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 716-1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (703) 716-1191
TELEFAX: (703) 716-1180
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 46.7.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 PNTREDLPYHYYDKK 326
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STATE: California
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Gaps

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Score 39; DB 1; Length 833; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lyamichey, James E.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          Length 833;
                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDION TYPE: COMPATION
WEDION TYPE: CIPOPPY disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PRE-BASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,043
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATONNEY/AGENT INFORMATION:
NAME: CARFOLL), Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: PORS-00613
TELEFRAK: 415/705-8410
TELEFRAK: 415/705-8410
                                                                                                                                                                                                                                                                                                            Score 39; DB 1; Pred. No. 1.4e+02; 4; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America 2DP: 94104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08483043 Patent No. 5691142
                     TELEPHONE: (415) 705-8410]
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 833 amino acids
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  527 PIVEKILOYRELTKLKN 543
                                                                                                                                                                                                                                                                                                                                                                                                         2 PVTQDDLQYHNLSKQQN 18
                                                                                                                                                            ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-254-359A-8
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                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
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Best Local Similarity
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APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MEDLEN & CRIVED FROM THERMOSTABLE
TITLE OF INVENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE
TITLE OF INVENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: 120 MOWGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COMPUTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTRY: IBM PC COMPATIBLE
COMPUTRY: IBM PC COMPATIBLE
COMPUTRY: IBM PC COMPATIBLE
COMPUTRY: IBM PC COMPATIBLE
COMPUTRY: SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.4e+02;
4; Mismatches 6; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,384C
FILING DATE: 04-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,359A
                                                                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CATTOLL, PETER G
REGISTATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FCKS-00613
FELECOMMUNICATION INFORMATION:
FELEPHONE: 415/39-838
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 833 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01000
                                                                                                                                                                                                                                                                                                               FORS-00613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08254359A Patent No. 5614402
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527 PIVEKILQYRELTKLKN 543
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MOLECULE TYPE: peptide
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            Gaps
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US-08-481-238

US-08-481-238

EACHLIANT DALICER, JAMES E.

APPLICANT: DALICERC, JAMES E.

APPLICANT: DALICERC, JAMES E.

APPLICANT: DALICERC, JAMES E.

APPLICANT: DALICERC, JAMES E.

APPLICANT: BROW, MARY ANN D.

TITLE OF INVENTION: SYNTHEELS-DEFICIENT THERMOSTABLE DNA TITLE OF INVENTION: POLYMERASE

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLES CARROLL

STATE: CALIFORNIA

COUNTRY: USA

CONFORTE RADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PREFENCY OF STEME COMPUTER: STATE: CALIFONNIA MEDIUM TYPE: PLOS/MS-DOS

SOFTWARE: PREFENCY OF STEME COMPATION:

TILING DATE:

CLASSIFICATION NUMBER: US/08/481,238

FILING DATE:

CLASSIFICATION NUMBER: 12,837

REFERENCE/DOCKET NUMBER: PERFE CALIFON:

NAME: CARROLL, PETER G.

TELEDHONE: (415) 705-8410

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION NUMBER: 32,837

TELECHONE CARROLL, PETER G.

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OR SED 1D NO: SEQUENCE CHARACTERISTICS:

LENGTH: 833 amino acid

STRANDEDERSS: SINGLE

TOPOLOGY: UNION OR SED 1D NO: SEQUENCE TYPE: PEPTION INFORMATION OR SED 1D NO: SEQUENCE TYPE: PEPTION OR SED 1D NO: SEQUENCE TYPE: PEPTION OR SED 1D NO: ASSET TYPE: MEDIUM OR SED 1D NO: ASSET TYPE: PEPTION OR SED 1D NO: ASSET TYPE: ASSET TYPE: PEPTION OR SED 1D NO: ASSET TYPE: ASSET TYPE: PEPTION OR SED 1D NO: ASSET TYPE: ASSET TYPE: PEPTION OR SED 1D NO: ASSET TYPE: ASSET TYPE: PEPTION OR SED 1D NO: ASSET TYPE: AS
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527 PIVEKILQYRELTKLKN 543
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Gaps ; Score 39; DB 1; Length 833; Pred. No. 1.4e+02; 4; Mismatches 6; Indels Query Match
Best Local Similarity 41.2%;
Matches 7; Conservative 2 PVTQDDLQYHNLSKQQN 18 ò

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Search completed: September 10, 2001, 14:01:56 Job time: 225 sec

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Human inducible ni human iNOS peptide Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Human secreted pro Fragment of human

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ALIGNMENTS
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AAW81263
AAW81292
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(without alignments)
16.268 Million cell updates/sec
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Compugen Ltd
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                                                                                                     September 10, 2001, 14:00:24
              GenCore version Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                            1 SPVTQDDLQYHNLSKQQN 18
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96
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Total number of

Searched:

Minimum DB Maximum DB

Perfect score:

Run on:

Sequence:

Scoring table:

Rat TNFR (p80) ext INFR:Fc fusion pro Plasmodium falcipa

Human secreted pro Human secreted pro Human ORFX ORF1331

Human secreted

Rat inducible nitr Human iNOS peptide Human iNOS peptide

Human secreted pro

Human 1NOS peptide fragment PS-5104. 30-APR-1999 (first entry) AAW81222;

Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.

Homo sapiens

/note= "Asn residue amidated" Location/Qualifiers 97WO-US06500 97US-6667777 Key Modified-site 11-APR-1997; WO9845710-A1 07-APR-1997; 15-0CT-1998

(WEBB/) WEBBER

Inducible nitric o Sequence encoded b Nitric-oxide-synth

AAW81222 AAW81178 AAW81204 AAW81204 AAW96322 AAR655764 AAR63206 AAR63206 AAR63206 AAR63206

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peptide (37-54) peptide peptide peptide

Human iNOS (Human iNOS (Human iNOS pHuman inos phuman

Description

DB

Length

Query Match]

Result Š

WPI; 1998-594495/50 Webber R;

us-08-833-506c-26.rag

Wed Sep 12 12:14:50 2001

A_Geneseq_0601:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or minics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inducible nitric oxide synthase; 1NOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                          This invention describes an immunoassay method where a sample with a
              Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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Pred. No. 1.1e-09;
Mismatches 0;
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                                                                                     Example 4; Page 35; 93pp; English.
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Best Local Similarity 100.
Matches 18; Conservative
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tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psorlasis, and multiple sclerosis. This sequence represents a peptide fragment from human iNOS which is used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes an immunoassay method where a sample with a specific blinding entity (e.g. a monoclonal antibody) readctive to human inducible nitric oxide synthase (iNoS) or mimics of this protein is used to detect the presence of human iNoS protein in the sample. The method can be used for the detection and quantitation of human iNOS in calls and tissues for various pathophyslological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following such as allows, psorlasis, and multiple solerosis. This sequence is allowed in monitoring "flare ups" in certain autoimmune diseases such as lupus, psorlasis, and multiple solerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.
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                                                                                                                                                                           Length 18;
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                                                                                                                                                                             100.0%; Score 96; DB 19; 100.0%; Pred. No. 1.1e-09;
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Pred. No. 1.1e-09;
                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      AAW81278 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human INOS peptide fragment #4.
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                                                                                                                                                                                           Local Similarity 100.
nes 18; Conservative
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                                                                                           of the invention.
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Matches

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RESULT

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This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence
                                                                                            Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis; Mab.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
                                                         Human iNOS peptide fragment capable of binding Mab 21C10-1D10 #2.
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                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence
                                                                                                                                                                                                                                                                                                              Inducible; nitric oxide synthase; 1NOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis; Mab.
   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 1.1e-09;
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100.0%;
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                                    1 SPVTQDDLQYHNLSKQQN 18
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Best Local Similarity 100.
Matches 18; Conservative
 Conservative
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AAW81208

Length 18; Indels

Ohneda M,

Clark SA,

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New human inducible nitric oxide synthase - useful for
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              93WO-US11401
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nes 18; Conservative
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                                                                        (UYPI-) UNIV PITTSBURGH
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                                                                                                                                    WPI; 1994-200273/24
                                                                                                                                                                                                                                                                                                                                                                                                            1153 AA;
                                                                                                                                                    N-PSDB; AAQ66914
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              23-NOV-1993;
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                                          25-NOV-1992;
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                                                                                                      Billiar TR,
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                                                                                                                                                                                                                                                                                                                                                                      Inhibition of cytokine mediated immunotoxicity of cells can be achieved by blocking free radical production or the accumulation of ree radicals in that cell. Treatment of insulin dependent diabetes mellitus (IDDM) can be achieved by by blocking nitric oxide (NO) production in a pancreatic beta cell and by providing a composition comprising an agent that reduces levels of fatty acids in the cells and protects beta-cells of the subject against lipid-mediated cell ceath. Cells can also be protected against nitric oxide mediated cytotoxicity by introducing into the cell an antioxidising agent. The methods can be used for protecting cells against immunotoxicity mediated by. e. g. IL-1 heta, IL-1 LI-3, IL-7, IL-7, IL-9, IL-17, C beta, IL-8, IL-17, IL-9, IL-17, IL-19, IL-17, IL-19, IL-17, C chmoattractant protein-1. The methods can be used for the treatment of e.g. insulin-dependent diabetes mellitus (IDDM, NIDDM, obesity, wasting syndromes, short stature, osteoporosis, inflammatory. cited is autoimmune diseases, or neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                      Protection of mammalian cells against immunotoxicity or lipotoxicity - used for treating, e.g. diabetes, obesity, wasting syndromes, osteoporosis, inflammatory diseases, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encoded by the cDNA clone for human hepatocyte inducible nitric oxide synthase.
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Pred. No. 1.4e-07;
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                                                                                                                                                                                Koyama K, Le
1, Thigpen A,
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ilarity 100.0%; P
Conservative 0;
                                                            98WO-US15781
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97US-0055092
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                                                                                                                                   (BETA-) BETAGENE INC.
(TEXA ) UNIV TEXAS SYSTEM.
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Best Local Similarity
These 18; Conserve
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N-PSDB; AAX08434.
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WO9906059-A2
                                                        30-JUL-1998;
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                            11-FEB-1999
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Sequence

à g AAR55764;

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CDNA
                                                                                                                                                                                                                                                                                                                                                        AAQ66914 is from human hepatocyte inducible nitric oxide synthase cDNA clone pHINOS from lambda Zap II cDNA library. The original source was induced human hepatocyte RNA. HINOS cDNA plasmid is pref. transformed in E. coli SOLK (ATCC 69126). The inventors claim a clone with the cDNA sequence in AAQ66914 and a cDNA clone which encodes AARS5764. The cloning and expression of a human tissue nitric oxide synthase cDNA provides a source of the enzyme for therapeutic purposes, for example to prevent the hypotensive shock seen with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                        cDNA clone encoding human inducible nitric oxide synthase - used to prevent the hypotensive shock seen with sepsis.
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Simmons RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 96; DB 15; 100.0%; Pred. No. 1.4e-07;
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Nussler AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR63206 standard; Protein; 1153 AA.
                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 53pp; English.
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Treatment of erectile dysfunction - by introducing an agent into penile tissue, particularly for inducing cavernosal smooth muscle relaxation or increasing NOS levels
                                                                                                                                                                                                                                         Nitric oxide synthetase; NOS; iNOS; HPINOS; human;
erectile dysfunction; impotence; gene therapy; corpora cavernosa;
                                                                                                                                                                                                            Human inducible nitric oxide synthetase.
                                                                                                                      AAW36113 standard; Protein; 1153 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 38-41; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GONZ/) GONZALEZ-CADAVID N F.
                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0017373.
                  1 SPVTQDDLQYHNLSKQQN 18
                                 11-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gonzalez-Cadavid NF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-008577/01.
N-PSDB; AAT98199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RAJF/) RAJFER J.
                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-1997;
                                                                                                                                                                                                                                                                                                                               W09742965-A1
                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                             20-NOV-1997.
                                                                                                                                                                                                                                                                        relaxant.
                                                                                                                                                   AAW36113;
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Matches
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                                                                                                                                                                                                                                                                    0;
                                                                                    nitric-oxide-synthase. CDNA was generated and used to construct a library in lambda ZAPII. This was screened with a 650 bp fragment of mouse inducible NO-synthase CDNA to identify the full-length clone pBSHSINOS. The insert was transferred to pSVL to give a vector capable of expressing NO-synthase in CHO cells under control of a heterologous constitutive promoter.
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An inducible nitric oxide syntase (iNOS = AAR88464) is the product of a CDNA clone (AAT10115) derived from human hepatocytes induced for iNOS biosynthesis. The iNOS can be obtd. by expression of the CDNA e.g. in mammalian host cells and is used in the development of selective inhibitors of NOS or to treat diseases
identifying enzyme inhibitors and stimulators, and for diagnosis and treatment of e.g. viral infections or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inducible nitric oxide synthase gene - useful in gene therapy to treat, e.g. vascular occlusive disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inducible nitric oxide synthase; iNOS; hepatocyte; gene therapy; vascular occlusive disease; cancer; infection.
                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                       Length 1153;
                                                                        Human chondrocytes were incubated with interleukin-1-beta to
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                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simmons RL,
                                                                                                                                                                                                                                      Score 96; DB 15;
Pred. No. 1.4e-07;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatocyte inducible nitric oxide synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 54-58; 91pp; English.
                                            Disclosure; Page 25-31; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nussler AK,
                                                                                                                                                                                                                                                                                                                                                                                                     AAR88464 standard; Protein; 1153 AA.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        affected by nitric oxide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-068641/07
                                                                                                                                                                                           1153 AA;
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Rajfer J;

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This protein comprises human penis inducible nitric oxide synthetase (HPiNOS). Its amino acid sequence was deduced from a cDNA clone (see AAT98199) derived from human penile smooth muscle cell mRNA. The invention is directed to a method of treating erectile dysfunction in a patient by providing an agent capable of treating erectile dysfunction, and introducing an effective amount of the agent into the penile tissue of the patient. Preferably, the agent increase in the level of NOS in tissue. Preferably, the NOS is iNOS, and the agent is introduced into the corpora cavernosa of the penis. The agent is preferably an NOS inducer, an NOS protein such as HPINOS, a cDNA encoding an NOS such as HPINOS, or CDNA transformed penile cells, especially corpora cavernosa
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100.0%; Pred. No. 1.4e-07;
iive 0; Mismatches 0;
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nes 18; Conser
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Gaps

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Indels

100.0%; Score 96; DB 17; 100.0%; Pred. No. 1.4e-07; iive 0; Mismatches 0;

Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative

Length 1153;

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Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoinmune disease; multiple sclerosis.
                                                                                                                                                                             Use of a nucleic acid delivery vehicle comprising a nucleic acid encoding nitric oxide synthase, especially useful in gene therapy for enhancing and/or inducing angiogenesis and treating atherosclerosis \cdot
                                                                                                                                                                                                                                                                                 The present invention relates to use of a nucleic acid delivery vehicle comprising a nucleic acid encoding nitric oxide synthase (NOS) activity for the manufacture of a composition for essentially isolated tissue perfusion treatment to enhance and/or induce anglogenesis. The nucleic acid delivery vehicle is particularly useful in gene therapy for the treatment of atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 96; DB 22; 100.0%; Pred. No. 1.4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                  Examples; Page 14-18; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human 1NOS peptide fragment PS-5261.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW81223 standard; peptide; 15 AA.
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                                      99EP-0202263.
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     99EP-0202263
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                                                                                                         Vogels R, Verlinden
                                                                          (INTR-) INTROGENE BV
                                                                                                                                            WPI; 2001-125729/14.
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Best Local Similarity
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     09-JUL-1999;
                                      09-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid delivery vehicle comprising a nucleic acid encoding nitric oxide synthase, used for isolated tissue perfusion treatment to enhance and induce anglogenesis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes a method for gene therapy for enhancing and inducing angiogenesis. The method uses a nucleic acid delivery vehicle, which comprises a nucleic acid encoding nitric oxide synthase (NOS). The delivery vehicle is used for the manufacture of a pharmaceutical composition for isolated tissue perfusion treatment. The method is useful for enhanching and/or inducing angiogenesis in patients with endothalial dysfunctions, in particular arteriosclerosis. The present sequence represents an inducible NOS.
                                                                                                         Amino acid sequence of a human inducible nitric oxide synthase (NOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                          Gene therapy; anglogenesis; nucleic acid delivery; arteriosclerosis;
nitric oxide synthase; NOS; endothelial dysfunction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 96; DB 22;
Pred. No. 1.4e-07;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human inducible nitric oxide synthase
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AAB31724 standard; Protein; 1153
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Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                            Verlinden SFF;
                                                                                                                                                                                                                                                                                                                                                                                         (INTR-) INTROGENE BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-123142/13.
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Matches 18; Conserv
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                                                                                                                                                                                               Homo sapiens.
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Sequence

Query Match

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represents a peptide from human iNOS which is used in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or minics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psorlasis, and multiple sclerosis. This sequence
                                   This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence impresents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inducible; nitric oxide synthase; iNOS; human; immunoassäy; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis; epitope mapping.
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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                                                                                                                                                                                                                                              84.4%; Score 81; DB 19; Length 15; 100.0%; Pred. No. 2.8e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human iNOS peptide fragment for epitope mapping #9.
              Example 4; Page 35; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 AAW81288 standard; peptide; 15 AA.
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                    4 TQDDLQYHNLSKQQN 18
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                                                                                                                                                                                                       15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (WEBB/) WEBBER
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                                                                                                                                                                              invention.
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                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes an immunoassay method where a sample with
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                                                                                                                       Length 15;
                                                                                                                                                                      Indels
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Pred. No. 4e-07;
                                                                                                                       DB 19; L
2.8e-07;
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                                                                                                        84.4%; Scc...
100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human iNOS peptide fragment PS-5104.
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                                                                                                                                                                                                                                                                                                                                                                                                   AAW81263 standard; peptide; 17 AA.
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                                                                                                                       Query Match 84.4
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                       4 TQDDLQYHNLSKQQN 18
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Modified-site
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invention
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1 SPVTQDDLQYHNLSKQQN 18 ||||||||||||||||| 1 spvtqddl-yhnlskqqn 17

Search completed: September 10, 2001, 14:00:24 Job time: 168 sec

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Q9khcl secondary e
Q9jyq8 neisseria m
Q9jtp9 neisseria m
Q9gcl xylella fas
Q66764 encephalomy
Q66763 encephalomy
Q66765 encephalomy
Q66766 encephalomy
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091vn5 pseudomonas
091vn5 pseudomonas
09620 streptomyce
09f8k2 carboxydoth
P74942 thermus aqu
067741 aquifex aeo
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Q9ule3 homo sapien
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007124 lactobacill
088063 streptomyce
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bacillus su
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Interpro: IPR003097; -- Interpro: IPR003097; -- Pfam; PF00667; FAD_binding; 1.
SEQUENCE 165 AA; 18466 MW; 99626E5FD04C2C3D CRC64;
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Q9JTP9
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Best Local Similarity 100."
Matches 18; Conservative
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   Homo sapiens (Human).
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   NCBI_TaxID=9606;
     094994
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09n175 ovis aries
09n2c9 equus cabal
09xt88 canis famil
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Q44568 acetobacter
Q9rws7 deinococus
Q9x1018 pseudomonas
Q9x1b1 thermotoga
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09s5z2 lactococcus
069936 streptomyce
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Q9r0w4 rattus norv
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Q9wtk6 cavia porce
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(without alignments)
32.830 Million cell updates/sec
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                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                       425026 seqs, 132305027 residues
                                                                                                                              September 10, 2001, 14:11:12
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                                                                                             OM protein - protein search, using sw model
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Q90w28
Q9R0w4
Q9N176
Q9ZPW1
Q9S5Z2
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Q9TUX8
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sp_rodent:*
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137 AA

PRT;

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Eukaryota; Metrzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INDGCABLE NITRIC OXIDE SYNTHASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 PALVQGILERVVDGPAP 47
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Best Local Similarity 94.1
Matches 16; Conservative
                                             PRELIMINARY;
                                                                                                                                                                                           Equus caballus (Horse).
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NON_TER
SEQUENCE
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                                                                 Q9N2C9;
                                             Q9N2C9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
Q9XT88
                       Q9N2C9
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Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                            SEQUENCE FROM N.A.
Ogawa Y., Nishijima S., Goto M., Ida M.;
Cloning and characterization of a novel splice valiant of human inducible nitric oxide synthase.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB022318; BAA37123.1;
HSSP; P35228; 4NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Mershon J.L., Clark K.E.; "Estrogen increases the expression of iNOS in the ovine coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

100.0%; Score 95; DB 4; Length 1114;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I artery.";
L Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF23342; AAF34710.1;
R InterPro: IPR001034;
R InterPro: IPR001034;
R InterPro: IPR001039;
R InterPro: IPR00309;
R InterPro: IPR00309;
R Ffam: PF00175; Oxidored_fad; 1.
PR Mm: PF00175; EAD_binding; 1.
PR Mm: PF00185; FANODOXIN.
PRINTS: PR00371; FPNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 94.7%; Score 90; DB 6; Length 945; Best Local Similarity 94.4%; Pred. No. 6.9e-06; Matches 17; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   1114 AA; 126748 MW; C1F9624774435571 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INDUCIBLE NITRIC OXIDE SYNTHASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   945 AA
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                                                                                                                                                                                                                              InterPro; IPR001094; -.
InterPro; IPR001034; -.
InterPro; IPR001709; -.
InterPro; IPR001709; -.
Pfam; PF00175; oxidored_fad; 1.
Pfam; PF00175; oxidored_fad; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PALVQGILERVVDGPTPH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PALVQGILERVVDGPTPH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                         NCBI_TaxID=9606;
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NON_TER
SEQUENCE
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Q9N175;
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09N175
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Gaps

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Length 137;

Score 82; DB 6; Length 137 Pred. No. 1.5e-05; 0; Mismatches 1; Indels

86.3%; 94.1%;

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SEQUENCE FROM N.A.
TISSUE-SPLENIC VEIN;
TESULCON D., Papapetropoulos A., Zhang X., Catravas J.D., Hintze T.H.,
Sessa W.C.;
                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
1NDGCIBLE NITRIC OXIDE SYNTHASE (FRAGMENT).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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88.2%; Pred. No. 0.00055;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF068682; AAD39341.1; -. HSSP; P35228; 1NSI.
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74304 MW; A645F80FFA9DBFB7 CRC64;
649 AA.
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InterPro; IPR003097; -.
Pro; Pro; FAD binding; 1.
PRINTS; PR00369; FLAVODOXIN.
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Matches 15; Conservative
  PRELIMINARY;
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1147 AA; 130625 MW; 2CAFB983E56F651A CRC64;
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Best Local Similarity
SEQUENCE
                                   Query Match
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XM MEDLINE-93221515; PubMed-7682072;

Wood E.R., Berger H.Jr., Sherman P.A., Lapetina E.G.;

Wood E.R., Berger H.Jr., Sherman P.A., Lapetina E.G.;

Therefore and macrophages express an identical cytokine inducible and nitric oxide synthase gene.";

Therefore Blooham. 191:767-774(1993).

R interpro; IPR001094; -...

R interpro; IPR001094; -...

R interpro; IPR001109; -...

R interpro; IPR001109; -...

R interpro; IPR001109; -...

R interpro; IPR001175; oxidored_fad; 1.

R fam; PF00175; oxidored_fad; 1.

R fam; PF00175; oxidored_fad; 1.

R Pfam; PR00175; PR00100371; PROR.

R PRINTS; RR003371; FROR.

R PRINTS; RR003371; FROR.

R PRODOM; PD001811; -; 1.
                                                                                                                                                            SEQUENCE FROM N.A.
TISSUB-AORTA;
MEDLINE-98431941; PubMed=9746458;
MEDLINE-98431941; PubMed=9746458;
Mang X., McGregor C.G.A., Miller V.M.;
"Induction and cDNA sequence of inducible nitric oxide synthase from canine aortic smooth muscle cells.";
Am. J. Physiol. 275:H1122-H1129(1998).
BENBL; AF077821; AAC78630.1; -.
HSSP; P29477; INOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                               Eukaryota; Metazoà; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                                                                                                                                                                                1154 AA; 131709 MW; 42CD606E447254CB CRC64;
                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
1NDUCIBLE NITRIC OXIDE SYNTHASE.
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYTOKINE INDUCIBLE NITRIC OXIDE SYNTHASE, INOS
                                                                                                                                                                                                                                                                                                                                                                                                    Score 60; DB 6
Pred. No. 0.56;
                                PRT; 1154 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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InterPro; IPR001433; ...
InterPro; IPR001709; ...
Pfam; PF00175; oxidored_fad; 1...
Pfam; PF00667; FAD_binding; 1...
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PRINTS; PR00371; FPNCR.
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Best Local Similarity 81.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             779 ALVQGILERVVYSPAP 794
                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ALVQGILERVVDGPTP 17
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                             097604
097604;
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Q9QW28;
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        RESULT
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                   097604
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEQUENCE FROM N.A.
STRAIN-WISTAR KYOTO;
MEDLINE-99326503; Pubwed-10395902;
Keinanen R.A., Vartiainen N., Koistinaho J.;
"Molecular cloning and characterization of the rat inducible nitric
                                                     ö
Score 59; DB 11; Length 1147;
Pred. No. 0.81;
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                                                     2; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                              PRT; 1147 AA.
                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00175; oxidored_fad; 1.
Pfam; PF00667; FAD_binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ230462; CAB46089.1; -
EMBL; AJ230465; CAB46089.1; JO
EMBL; AJ230466; CAB46089.1; JO
EMBL; AJ230466; CAB46089.1; JO
EMBL; AJ230466; CAB46089.1; JO
EMBL; AJ230469; CAB46089.1; JO
EMBL; AJ230470; CAB46089.1; JO
EMBL; AJ230471; CAB46089.1; JO
EMBL; AJ230472; CAB46089.1; JO
EMBL; AJ230472; CAB46089.1; JO
EMBL; AJ230474; CAB46089.1; JO
EMBL; AJ230479; CAB46089.1; JO
EMBL; AJ230481; CAB46089.1; JO
EMBL; AJ230485; CAB46089.1; JO
EMBL; AJ230485; CAB46089.1; JO
EMBL; AJ230485; CAB46089.1; JO
EMBL; AJ230481; CAB46089.1; JO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oxide synthase (iNOS) gene.";
Gene 234:297-305(1999).
     62.1%;
81.2%;
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80.0%;
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PRINTS; PR00371; FPNCR.
                                                                                                                               779 ALVQGILERVVDCSSP 794
                         Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                      2 ALVQGILERVVDGPTP 17
                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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Gaps

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Indels

Matches

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Lactococcus lactis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99194715; PubMed=10094684; MEDLINE-99194715; PubMed=10094684; Ingmer H., Vogensen F.K., Hammer K., Kilstrup M.; Ingmer H., Vogensen F.K., Hammer K., Kilstrup M.; Disruption and analysis of the cipB, cipC, and cipE genes in bacteria...; J. Bacteria...; J. Bacteria...; J. Bacteria...; J. Bacteria...; J. RAP01919182.1; -... InterPro; IPR001939; -... InterPro; IPR001939; -...
                                                                                                                                Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Length 748;
InterPro; IPR000007; -.
Pfam; PF01167; Tub; 1.
PR051TE; PS01200; TUB_1; UNKNOWN_1.
PROSITE; PS01201; TUB_2; UNKNOWN_1.
SEQUENCE 386 AA; 43092 MW; 65BBBDE7851237FA CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CLP PROTEASE ATP BINDING SUBUNIT
                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                            Score 47; DB 10;
Pred. No. 20;
3; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 2
Pred. No. 42;
6; Mismatches
                                                                                                                                                                                                                                                                                                                             748 AA
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                                                                                                                            49.5%;
                                                                                                                                                                                                                       1::|||| | |:|
254 PSVVQGIEEEVSSSPSP 270
                                                                                                                                                                                                  1 PALVOGILERVVDGPTP 17
                                                                                                                            Query Match 49.5
Best Local Similarity 52.9
Matches 9; Conservative
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160 AVVEGLAQKIVDGDVP 175
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                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001943; -.
InterPro; IPR003593; -.
Pfam; PF00004; AAA; 2.
Pfam; PF02151; UVR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       748 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-MG1363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                           Q9S5Z2
Q9S5Z2;
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                                                                                                                                                                                                                                                                                         RESULT 11
09S522
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Matches
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069936
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     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thallana (Mouse-ear cress).
Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Brassloaphyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassloales; Brassloaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                    Ovis aries (Sheep).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-V. COLUMBLA,
Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.,
Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.;
"Arabidopsis thaliana chromosome II BAC T30D6 genomic sequence.";
Submitted (FRB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006439; AAD15508.1; -.
                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
Mershon J.L., Clark K.E.;
Mershon J.L., Clark K.E.;
"Estrogen increases the expression of INOS in the ovine coronary
"Estrogen increases the expression of INOS in the ovine coronary
     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6;
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Pred. No. 19;
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  artery";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AAF23471; AAF34707.1;
InterPro; IPR001433;
InterPro; IPR001709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366 366
366 Aa; 40791 MW; 794B274DA786A4A0 CRC64;
                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ENDOTHELIAL NITRIC OXIDE SYNTHASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY 1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
PUTATIVE TUBBY PROTEIN.
     ;
                                                                                                                                                               366 AA
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     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00175; oxidored_fad; 1.
Pfam; PF00667; PAD_binding; 1.
PRINTS; PR00371; FPNCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PALVQGILERVVDGPTP 17
12; Conservative
                                                                                                                                                               PRELIMINARY;
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                                                         111111111 :1
780 LVQGILERVVDCSSP 794
                                   3 LVQGILERVVDGPTP 17
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SEQUENCE
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09N176;
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Q92PW1 RESULT 10

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Gaps

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Pfam; PF00667; FAD_binding; 1. PRINTS; PR00369; FLAVODOXIN. PRINTS, PR00371; FPNCR. SEQUENCE 1205 AA; 133045 MW.
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Harris D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                       RESULT 14
Q9WTK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
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1D 0.09FBQE
0.09FBQE
0.09FBQE
0.09FBGE
0.00FBGE
0.00C 0.0
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                                                                                                                                                                                                                                                                                                Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicalor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL; AL023661; CAA19619.1; -.

InterPro; IPR001279; -.

InterPro; IPR001939; -.

InterPro; IPR001943; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 842;
                                                        STRAIN=A3(2);
Oliver K., Harris D.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                              Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               842 AA; 92110 MW; A8ADC12FDA90197F CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB
Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=HEART;
MEDLINE=99369487; PubMed=10442857;
                                                                                                                                                                                                                                                               STRAIN=A3(2);
MEDLINE=97000351; Pubmed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloning.";
Nitric Oxide 3:254-264(1999).
EMBL; AFL43503; AAD52161.1; -.
HSSP; P29474; 3NOS.
InterPro; IPR001094; -.
X InterPro; IPR0011709; -.
X InterPro; IPR001709; -.
R InterPro; IPR003097; -.
R InterPro; IPR003097; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00175; oxidored_fad; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00300; CLPPROTEASEA.
PROSITE; PS00870; CLPAB_1; 1.
PROSITE; PS00871; CLPAB_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.5%;
illarity 43.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2000 (TrEMBLrel. 15, NITRIC OXIDE SYNTHASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003593; -. Pfam; PF00004; AAA; 2. Pfam; PF02151; UVR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00382; AAA; 1.
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Best Local Similarity
Matches 7; Conserv
                                       SEQUENCE FROM N.A.
                                                                                                                                         SEQUENCE FROM N.A.
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NCBI_TaxID=1902;
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                                                                                                                                                           STRAIN=A3(2);
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SEQUENCE
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                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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                                                               Length 1205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Derst C., Preisig-Mueller R., Rajan S., Daut J.;

"Cloning and sequencing of guinea pig NO synthases.";

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF146041; AAD29753.1;

EMBL, AF146040; AAD29753.1;
133045 MW; C150CDEB01685BA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EB4E792D3F9503DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SCD866.01C.
                                                                    .
9
                                                               Score 47; DB 6
Pred. No. 72;
2; Mismatches
                                                                                                                                                                                                                                                                                                           PRT; 1206 AA.
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                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Create 01-NOV-1999 (TrEMBLrel. 12, Last s 01-MAR-2001 (TrEMBLrel. 16, Last a ENDOTHELIAL NITRIC OXIDE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P29474; 3NOS.
InterPro; IPR001094; -.
InterPro; IPR001433; -.
InterPro; IPR001709; -.
InterPro; IPR003097; -.
Pfam; PF00175; oxidored_fad; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133692 MW;
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                                                                 49.5%;
52.9%;
                                                                                                                                                                                   809 PGLVEALLSRVEDPPPP 825
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Best Local Similarity 52.9,
Conservative
                                                                                                                                                     1 PALVQGILERVVDGPTP 17
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Best Local Similarity 52.9
Matches 9; Conservative
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RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

RN [2]
RN [2]
RA SEQUENCE FROM N.A.
RA Gerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RN Gradeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RN SEQUENCE FROM N.A.

RN MEDLINE-97000351; Pubmed-8843436;
RX MIGRAPH M.Y. Denapaite D., Eichner A., Cullum J., RT A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RY "A set of ordered cosmids and a detailed genetic and physical map for KT "A set of ordered cosmids and a detailed genetic and physical map for KT Transferase.

RY "A set of Ordered Cosmids and a detailed genetic and physical map for KT Transferase.

RY Transferase.

RY Transferase.

FY NON_TER 100 A3; 10559 MW; 2AE37FE5F3976A79 CRC64;

QUETY MATCh

QUETY MATCh

QUETY MATCh

Best Local Similarity 52.4%; Pred. No. 5.3;

MAtches 11; Conservative 2; Mismatches 5; Indels 3; Gaps 1;
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Search completed: September 10, 2001, 14:11:13 Job time: 592 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:09:52; Search time 23.82 Seconds

(without alignments)
25.886 Million cell updates/sec
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Title: US-08-833-506C-30
Perfect score: 95
Sequence: 1 PALVQGILERVVDGPTPH 18

ice: 1 PALVQGILERVVDGPTPH

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SUMMARIES	
Result		Query				
No.	Score	Match	Match Length	DB	O.	Description
1	95	100.0	1153	-	NS2A_HUMAN	P35228 homo sapien
7	79	83.2	1144	Ч	NOS2_MOUSE	mus n
e	74	77.9	1149	-	NOS2_CAVPO	054705 cavia porce
4	59	62.1	1147	-	NOS2_RAT	
2	59		1147	Н	NS2D_HUMAN	O60591 homo sapien
9		7	496	٦	NOS2_RABIT	019114 oryctolagus
7	49	÷	1217	Н	YHCR_BACSU	~
80	48	50.5	1202	Н	NOS3_HUMAN	
6	47	49.5	1204	7	NOS3_BOVIN	<u>-</u>
10	46	48.4	826	П	CLPB_HAEIN	P44403 haemophilus
11	46	48.4	2290	П	POLG_EMCV	4
12	46	48.4	2292	П	POLG_EMCVB	
13	₹	48.4	2292	П	POLG_EMCVD	
14	45.5	47.9	369	_	MURB_MYCTU	<u>~</u>
15	45	47.4	857	7	CLPB_ECOLI	
16	44	46.3	911	П	H101_ARATH	0
17	43	45.3	637	٦	YHES_ECOLI	
18	43	45.3	848	Н	CLPB_MYCTU	
19	43	45.3	878	7	CLPB_TREPA	_
20	43	45.3	806	7	H104_YEAST	saccha
21	43	45.3	1136	П	NOS2_CHICK	-
22	43		1165	П	PEX6_PICPA	pichia
23	42	•	763	П	CLPL_LACLA	lactoco
24	42		811	_	HSP7_YEAST	
25	41		333	-	PEPR_LACDL	Q48544 lactobacill
56	41		467	-	INVO_MOUSE	P48997 mus musculu
27	41		504	П	DCMC_ANSAN	P12617 anser anser
28	41	43.2	530	-	HMA2_ARATH	P49294 arabidopsis
29	41	43.2	852	7	CLPB_CORGL	P53532 corynebacte
30	41	43.2	868	1	CLP_TRYBB	P31543 trypanosoma
31	41	43.2	883	-	CLPB_SYNP7	P53533 synechococc
32	41	43.2	919	П	NOS3_RAT	Q62600 rattus norv
33	41	43.2	1201	П	NOS3_MOUSE	P70313 mus musculu

Q00746 emericella P04760 mus musculu p18916 rattus norv Q63651 rattus norv Q13472 homo saplen P33459 caprine art P2338 r multiphos P49327 homo saplen P12785 rattus norv P28941 equine herp P08246 homo saplen P34072 saccharomyc
ANG1_EMENI ACHG_RAT ACHG_RAT TP3A_HUMAN POT_CAEVC PTI_RHOCA FAS_HUMAN FAS_HUMAN FAS_RAT VGLL_HSVEB ELNE_HUMAN MKS1_YEAST
277 519 519 564 1001 1109 827 2505 218 267 584
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9
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ALIGNMENTS

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"Structural characterization of nitric oxide synthase isoforms reveals striking active-site conservation.";
Nat. Struct. Biol. 6:233-242(1999).
-I- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 74-504.
MEDLINE-99340067; Pubmed-10409685;
Lid H., Raman C.S., Glaser C.B., Blasko E., Young T.A., Parkinson J.F.,
Whitlow M., Poulos T.L.;
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                                     TISSUE-Glioblastoma; MEDLINE-9515567; PubMed-7531687; MeDLINE-9515567; PubMed-7531687; Medrar A., Zentya M., Esumi H.; "Cloning and functional expression of human inducible nitric oxide synthase (NOS) cDNA from a glioblastoma cell line A-172."; J. Blochem. 116:575-581(1994).
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MEDLINE-97304504; PubMed=9160867;
Luss H., Li R.-K., Shapiro R.A., Tzeng E., McGowan F.X., Yoneyama Hatakayama K., Geller D.A., Mickle D.A.G., Simmons R.L.,
Billiar T.R.;
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MEDLINE-99173237; PubMed-10074942;
Estchmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,
Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,
Weber P.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
MEDLINE-983865; Pubmed-9721329;
TAJLOR B.S., ABCOD L.H., Bllliar T.R.;
Inducible nitric oxide synthase in the liver: regulation and
                                                                                                                                                                                                            in normal human airway epithelium in vivo.";
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MEDLINE-95165725; PubMed-7532248;
                                                                                                                                             TISSUE∽Airway epithelium;
MEDLINE⇔95372368; PubMed⇔7544004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunomodulatory mechanism?";
Kidney Int. 46:1043-1049(1994).
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 380-473 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biokhimiia 63:766-781(1998).
                       SEQUENCE FROM N.A.
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Blochem.
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                                                                                                                                                        THE ENZYME (BY SIMILARITY).

ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST WITH MOUSE NOS2). ASPIRIN INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND BEFECTS MAY BE EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY SIMILARITY).

SUBGUIT: HOMODIMER:

TISSUE SPECIFICITY: EXPRESSED IN THE LIVER, RETINA, BONE CELLS AND AIRMAY EPITHELIAL CELLS OF THE LING. NOT EXPRESSED IN THE
                      MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.

CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) ~ CITRULLINE + NITIC OXIDE + N NADP(+).

COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding; Heme; Phosphorylation; Zinc; Metal-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CALMODULIN-BINDING (POTENTIAL).
FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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IN MACROPHAGES, NO
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NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES
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EMBL, X73029; CAA51512.1; --
EMBL, W05810; AAA56665.1; --
EMBL, U05810; AAA56666.1; --
EMBL, U31511; AAA49041.1; --
EMBL, U20141; AAB603366.1; --
EMBL, WARNERS W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR003097; -. Pfam; PF00667; FAD_binding; 1. Pfam; PF00175; oxidored_fad; 1. PRINTS; PR00369; FLAVODOXIN. PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; S75615; AAD14179.1;
A47475; A47475.
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2NSI; 07-JAN-00.
4NOS; 04-FEB-00.
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MEDLINE=20031637; PubMed=10562538;
Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhui R., Crooks C.,
Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.;
"Inducible nitric oxide synthase: role of the N-terminal beta-hairpin hook and pterin-binding segment in dimerization and
                                                                                                                                                                                                                                                                                                              Xie Q.-W., Cho H.J., Calaycay J., Mumford R.A., Swiderek K.M.,
Lee T.D., Ding A., Troso T., Nathan C.;
"Cloning and characterization of inducible nitric oxide synthase from
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92357701; PubMed=1379716;
Lowenstein C.J., Glatt C.S., Bredt D.S., Snyder S.H.;
"Cloned and expressed macrophage nitric oxide synthase contrasts with
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SEQUENCE FROM N.A.
GTRAIN-DBA/2J, BALB/CBYJ, SJL/J, NOD/LIJ, AND B10.S/J; TISSUE-Spleen;
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92210618; PubMed-1372907;
Lyons C.R., Orloff G.J., Cunningham J.M.;
"Molecular cloning and functional expression of an inducible nitric
oxide synthase from a murine macrophage cell line.";
J. Biol. Chem. 267:6370-6374(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97477482; pubMed=9334294;
Crane B.R., Arval A.S., Gachhui R., Wu C., Ghosh D.K., Getzoff E.D. Stuehr D.J., Tainer J.A.;
"The structure of nitric oxide synthase oxygenase domain and inhibitor complexes.";
                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96088781; PubMed-7503239;
Kone B.C., Schwoebel J., Turner P., Mohaupt M.G., Cangro C.B.;
"Role of NF-kappa B in the regulation of inducible nitric oxide
synthase in an MTAL cell line."
                                                                                                                                              P29477; 070515; 070516; 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC OXIDE SYMTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
(INDUCIBLE NOS) (INOS) (MACROPHAGE NOS) (MAC-NOS).
                                ö
        Length 1153;
                               Indels
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
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        Score 95; DB 1; I
Pred. No. 7.1e-08;
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                                                                                                                                       PRT; 1144 AA
                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Am. J. Physiol. 269:F718-F729(1995)
                                                                                                                                                                                                                                                                                                     MEDLINE=92229444; PubMed=1373522;
       Query Match 100.0%; Some Best Local Similarity 100.0%; P. Matches 18; Conservative 0;
                                                                    1 PALVQGILERVVDGPTPH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 278:425-431(1997).
                                                                                                                                                                                                                                                                                                                                                  mouse macrophages.";
Science 256:225-228(1992).
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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NOS2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oxide synthase.";

Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).

Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).

-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.

-!- CATALLYTIC ACTIVITY: L.-ARGININE + N NADPH + M O(2) - CITRULLINE + NITRIC OXIDE + N NADP(+).

-!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Macrophage;
MEDLINE-95372392; PubMed=7544010;
ARDLINE-95372392; Attur M., Leszczynska-Piziak J., Patel I.R.,
Manin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,
Weissmann G., Abramson S.B.;
"The mode of action of aspirin-like drugs: effect on inducible nitric
                                                                                                                                                                                           Stuehr D.J.,
                                                                                                                                                                                                                                      Structure of nitric oxide synthase oxygenase dimer with pterin and unbarrate ^{\mathrm{n}} .
                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.

WEDLINE-20031638 PubMed-10562539.

Crane B.R., Rosenfeld R.J., Arvai A.S., Ghosh D.K., Ghosh S.,

Tainer J.A., Stuehr D.J., Getzoff E.D.;

The terminal domain swapping and metal ion binding in nitric oxide synthase dimerization."

Synthase dimerization."

EMBO J. 18:6271-6281(1999).
                                                                                                         X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.
MEDLINE-98182450; PubMed-9516116;
Crane B.R., Arval A.S., Ghosh D.K., Wu C., Getzoff E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUBUNIT: HOMODIMER.
-:- TSSUE SPECIFICITY: MACROPHAGES.
-:- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES.
-:- SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY
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EMBL, AF065920; AAC17915.1; -.
EMBL, AF065921; AAC17915.2; -.
EMBL, AF065923; AAC17917.1; ALT_INIT.
EMBL, AF05592; AAC17918.2; -.
PIR; A43271; A43271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M92649; -; NOT_ANNOTATED_CDS.
M84373; AAA39834.1; -.
U43428; AAC52356.1; -.
tetrahydrobiopterin interaction.";
EMBO J. 18:6260-6270(1999).
                                                                                                                                                                                                                                                                                                                                            Science 279:2121-2126(1998).
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1NOS; 18-NOV-98.
2NOS; 18-NOV-98.
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04-FEB-00.
06-FEB-00.
06-FEB-00.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oxide synthase."
                                                                                                                                                                                                                                  rainer J.A.;
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                                                                                                                                                                                                                                                                                                             substrate.
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-i - TISSUE SPECIFICITY: EXPRESSED IN THE LUNG AND COLON. NOT DETECTED
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BINDING 199
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SEQUENCE
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NP_BIND
NP_BIND
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NP_BIND
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COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF THE ENZYME (BY SIMILARIY).

ENZYME (BY SIMILARIY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
                                                 MGD; MGI: y, y, w, m, the proof of the proof
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C -> R (IN STRAIN NOD/LTJ).
P -> L (IN STRAIN SJL/J).
S -> F (IN STRAIN BALB/CBYJ).
K -> T (IN REF. 4).
A -> V (IN REF. 2).
A -> G (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZINC.
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94.18;
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990
1085
104
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211
967
968
                        1DD7; 29-MAR-00.
MGI:97361; Nos2.
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Best Local Similarity
Matches 16; Conserv
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054705;
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NP_BIND
NP_BIND
NP_BIND
NP_BIND
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VARIANT
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DRAMAN AND THE FET THE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@license.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CALMODULIN-BINDING (POTENTIAL).
FWN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
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BEDELINE-S1919121; Pubmed-7680561;

Nunckawa Y., Ishida N., Tanaba S.;

"Cloning of Inducible nitric oxide synthase in rat vascular smooth
IN THE HEART, AORTA, LIVER, KIDNEY, AND SPLEEN.
--- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS) IN KIDNEY, SPLEEN, AN COLON. EXPRESSION IS REDUCED IN THE PRESENCE OF LPS IN LUNG.
---- SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN "WISTAR; TISSUE "Pancreatic islets; MEDLINE-95309542; PubMed" 7540573; Karlsen A.E., Andersen H.U., Vissing H., Larsen P.M., Fey S.J., Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ξ
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.. 0.00022;
... 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 191:89-94(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 74; DB 1;
Pred. No. 0.00022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00667; FAD_binding; 1. Pfam; PF00175; oxidored_fad; 1.
                                                                                                                                                                                                                                                                                                           EMBL; AF027180; AAC33177.1; -.
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83.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130631
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Matches 15; Conservative
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199
528
653
777
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InterPro; IPR001094; -.
InterPro; IPR001433; -.
InterPro; IPR001709; -.
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SEQUENCE OF 426-788 FROM N.A.
STRAIN-DAHL/RAPP SALT SENSITIVE STRAIN; TISSUE-Vascular smooth muscle;
MEDLINE-98195092; PubMed-9535415;
Chen P.Y., Gladish R.D., Sanders P.W.;
"Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SPRAGUE-DAWLEY, TISSUE-Aorta;
MEDLINE-94325351; PubMed-7519448;
Geng Y.J., Almquist M., Hansson G.K.;
"CDNA cloning and expression of inducible nitric oxide synthase from rat vascular smooth muscle cells.";
Blochim. Biophys. Acta 1218:421-424(1994).
                                                                                                                                                                                                                                                                                         STRAIN-SPRAGUE DAWLEY, TISSUE-Hepatocytes;
MEDLINE-93221515; PubMed-7682072;
Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
"Hepatocytes and macrophages express an identical cytokine inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97070590; PubMed-8913516;
Tsutsumishita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,
Futati S., Niwa M.;
Sequence analysis of inducible nitric oxide synthase in rat kidney,
lung, and uterus:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-WISTAR; TISSUE-Renal glomerulus;
Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S.;
"Advances in the studies of NO synthesis regulation in mesanglial
cells.";
Mandrup-Poulsen T., Boel E., Nerup J.; "Clonding and expression of cytokine-inducible nitric oxide synthase CDNA from rat islats of Langerhans."; Diabetes 44:753-758(1995).
                                                                      STRAIN=SPRAGUE-DAWLEY; TISSUE-Astrocytes;
MEDLINE-9421594; PubMed-7513765;
Galea E., Reis D.J., Feinstein D.L.;
"Cloning and expression of inducible nitric oxide synthase from rat
                                                                                                                                                                                           Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K., Kawasaki H., Sugimura T., Esumi H.;
"Molecular cloning of a cDNA encoding an inducible calmodulin-dependent nitric-oxide synthase from rat liver and its expression in COS 1 cells.";
Eur. J. Blochem. 217:37-43(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morrissey J.J., McCracken R., Kaneto H., Vehaskari M., Montani D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kosuga K., Yui Y., Hattori R., Sase K., Eizawa H., Aoyama 'Inoue R., Sasayama S.;
Iroue R., Sasayama S.;
Cloning of an inducible nitric oxide synthase from rat polymorphonuclear neutrophils.";
Endothelium 2:217-221(1994).
                                                                                                                                                                                                                                                                                                                                            nitric oxide synthase gene.";
Biochem. Biophys. Res. Commun. 191:767-774(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SPRAGUE-DAWLEY; TISSUE-Renal glomerulus; MEDLINE-94276509; PubMed-7516453;
                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lung, and uterus.";
Biol. Pharm. Bull. 19:1374-1376(1996).
                                                                                                                      astrocytes.";
J. Neurosci. Res. 37:406-414(1994).
                                                                                                                                                                               MEDLINE-94039059; PubMed-7693462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypertension 31:918-924(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           salt-sensitive rats.
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                                                                                                                                                                ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN HINBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CAPALYTIC ACTIVITY (BY
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CALMODULIN-BINDING (POTENTIAL).
FAM (PYRINIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIGOSE PART) (BY SIMILARITY).
ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                         -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMODIMER (BY SIMILARITY).

TISSUE SPECIFICITY: IN NORMAL KIDNEY, EXPRESSED PRIMARILY IN THE MEDULLARY THICK ASCENDING LIMB, WITH MINOR AMOUNTS IN THE MEDULLARY COLLECTING DUCT AND VASA RECTA BUNDLE.

INDUCTION: BY INTERFERENC GAMMA AND LIPOPOLYSACCHARIDE.
SIMILARITY: BELONGS TO THE NOS FAMILY.
Klahr S.; "Location of an inducible nitric oxide synthase mRNA in the normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00667; FAL_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNC.
Oxidoreductase; NADP; FAD; FWN; Calmodulin-binding; Heme; Zinc; Metal-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L12562; AAA41720.1; EMBL; X76881; CAA54208.1; EMBL; D44591; BAA07994.1; EMBL; D83661; BAA12035.1; EMBL; AF006619; AAC16401.1; EMBL; U48829; AAB18620.1; EMBL; S71597; AAB31028.2; EMBL; L36063; AAC02242.1; ---
                                                                    Kidney Int. 45:998-1005(1994).
                                                                                                                     SEQUENCE OF 420-479 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, D14051; BAA03138.1; -. EMBL, U026686. AAA85861.1; -. EMBL; U03699; AAC13747.1; -. EMBL; D12520; BAA02090.1; -.
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Interpro; IPR001433; -.
Interpro; IPR001709; -.
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                                                                                                                                              TISSUE-Myocardium;
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SEQUENCE FROM N.A.
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-I FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO MEDIATES TUMORICIDAL ADD BACTERICIDAL ACTIONS. MAY BE INVOLVED IN THE PATHOGENESIS OF DILATED CARDIOMYOPATHY OR OF EXERCISE INVOLERANCE OBSERVED IN PATERYS WITH CHRONIC HEART FAILURE.

-I CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) ·· CITRULLINE + NITRIC OXIDE + N NADP(+).

-I COPPACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FWN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF THE ENZYME (BY SIKILARIY).
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060591; 060604;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
NITRIC OXIDE SYNTHASE, INDUCIBLE IID (EC 1.14.13.39) (NOS, TYPE II (INDUCIBLE NOS) (INOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete coding sequence of inducible nitric oxide synthase from human heart and skeletal muscle of patients with chronic heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Adams V., Krabbes S., Jiang H., Yu J., Rahmel A., Gielen S.,
Schuler G., Hambrecht R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59; DB 1; Length 1147; Pred. No. 0.071;
                                                                                                                                                           7 AND 8).
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(IN REF. 5 AND 9).

(IN REF. 11).

(IN REF. 1 AND 6).

(IN REF. 2).

(IN REF. 10).
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G -> A (II
G -> V (II
A -> R (II
D -> G (II
ET -> VP
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Matches 13; Conservative
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                                                                                                                            Homo sapiens (Human).
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              CONFLICT
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NS2D_HUMAN
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-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- TISSUE SPECIFICITY: EXPRESSED IN THE HEART AND SKELETAL MUSCLE
-i-TISSUE SPECIFICITY: EXPRESSED IN THE HEART AND SKELETAL MUSCLE
-i- SIMILARITY: BELONGS TO THE NOS FAMILY.
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae; Oryctolagus.
NCBI_TaxID-9986;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
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InterPro; IPR001433; --
InterPro; IPR001433; --
InterPro; IPR001709; --
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
PRINTS; PR00369; FENCR.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92340475; PubMed-1378832; Janssens S.P., Shimouchi A., Quertermous T., Bloch D.B., Bloch K.D.; "Cloning and expression of a cDNA encoding human endothellum-derived trelaxing factor/nitric oxide synthase."; J. Biol. Chem. 267:14519-14522(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Janssens S.P., Shimouchi A., Quertermous T., Bloch D.B., Bloch K.D., J. Biol. Chem. 267:22694-22694(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=92354731; PubMed=1379542;
Marsden P.A., Schappert K.T., Chen H.S., Flowers M., Sundell C.L.,
Wilcox J.N., Lamas S., Michel T.;
Molecular cloning and characterization of human endothelial nitric
oxide synthase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marsden P.A., Heng H.H., Scherer S.W., Stewart R.J., Hall A.V., Shi X.M., Tsui L.C., Schappert K.T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                        51.6%; Score 49; DB 1; Length 1217; 64.3%; Pred. No. 3.6; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                     Pfam; PF01000; 5_nucleotidase; 1.
Pfam; PF010746; Gram_pos_anchor; 1.
Pfam; PF00746; Snase; 1.
PROSITE; PS00786; 5_NUCLEOTIDASE_1; FALSE_NEG.
PROSITE; PS00786; 5_NUCLEOTIDASE_2; 1.
Hypothetical protein; Hydrolase.
SEQUENCE 1217 AA; 132686 MW; 7973160CC898DCOB CRC64;
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MEDLINE-93352539; PubMed-7688726;
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                                                                                                                                                           EMBL; X96983; CAA65702.1; -. EMBL; Z99108; CAB12747.1; -.
                                                                                                                                                                                                          Subtilist; BG11596; yhcR.
InterPro; IPR000080; -.
InterPro; IPR001899; -.
InterPro; IPR00224; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 64.3
Matches 9; Conservative
 NUCLEOTIDASE FAMILY.
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379 EGIVDRVVDGDTIH 392
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(FLAVIN PART) (BY SIMÎLARITY).
? (RIBOSE PART) (BY SIMÎLARITY).
? (ADP PART) (BY SIMÎLARITY).
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01-ocr-1996 (Rel. 34, Last sequence update)
01-ocr-1996 (Rel. 39, Last sequence update)
39. MAY-2000 (Rel. 39, Last monctation update)
HYPOTHETICAL 132.7 KDA PROTEIN IN CSPB-GLPP INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 496;
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Pred. No. 0.13;
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STRAIN-NEW ZEALAND WHITE; TISSUE-Heart;
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FAD (2
FAD (1
NADP
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SIMILARITY: BELONGS TO THE NOS FAMILY
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 "Expression of constitutive endothelial nitric oxide synthase in human blood platelets."; Life Sci. 57:2049-2055(1995). [10]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT CORONARY SPASM ASP-297.
MEDILNE-98407797, Pubbled-9737779;
Yoshimura M., Yasue H., Nakayama M., Shimasaki Y., Sumida H.,
Sugiyama S., Kugiyama K., Ogawa H., Ogawa Y., Saito Y., Miyamoto Y.,
                                                                                                          Nadaud S.A., Bonnardeaux A., Lathrop M., Soubrier F.; Gene structure, polymorphism and mapping of the human endothelial nitric oxide synthase gene.": 198:1027-1033(1994).
                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
MEDLINE-99173237; PubWed-10074942;
Hischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,
Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,
Weber P.C.;
"Structure and chromosomal localization of the human constitutive endothelial nitric oxide synthase gene."; J. Biol. Chem. 268:17478-17488(1993).
                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-9433373; PubMed-7519987;
MIDALINE-9433373; PubMed-7519987;
Mighara K., Kawamoto T., Sase K., Yui Y., Toda K., Yang L.X.,
Hattorl K., Aoyama T., Yamamoto Y., Doi Y., Ogoshi S.,
Hashimoto K., Kawai C., Sasayama S., Shizuta Y.;
"Cloning and structural characterization of the human endothelial
                                                                                                                                                                                                                                                            Robinson L.J., Weremowicz S., Morton C.C., Michel T.;
"Isolation and chromosomal localization of the human endothelial nitric oxide synthase (NOS3) gene.";
Genomics 19:350-357(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural characterization of nitric oxide synthase isoforms reveals striking active-site conservation."; Nat. Struct. Biol. 6:233-242(1999).
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-i- SUBUNIT: HOMODIMER.
-i- TISSUE SPECIFICITY:
-i- DISEASE: DEFECTS IN NOS3 ARE INVOLVED IN CORONARY SPASM.
                                                     Liao J.K.;
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                             nitric-oxide-synthase gene.";
Eur. J. Biochem. 223:719-726(1994).
                                                                                        TISSUE-Placenta;
MEDLINE-94161710; PubMed-7509596;
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                                   SEQUENCE FROM N.A.
TISSUE ∪ Umbilical vein;
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FAN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
MYRISTATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
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InterPro; IPR001433; -..
InterPro; IPR001433; -..
InterPro; IPR001709; -..
Pfam; PF00667; FAD_binding; 1..
Pfam; PF00175; oxidored_fad; 1..
PRINTS; PR00369; FLAVODOXIN.
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EMBL; X76314; CAA53950.1; JC
EMBL; X76315; CAA53950.1; JC
EMBL; X76316; CAA53950.1; JC
EMBL; D26607; BAA05652.1; -
EMBL; L23210; AAA36373.1; -
EMBL; S80791; AAD14336.1; -
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X76312; CAA53950.1;
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PIR; A42867, A42867.
PDB; 3NOS; 04-FEB-00.
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01-JUL-1993 (Rel. 26, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC-OXIDE SYMTHASE, ENDOTHELIAL (EC 1.14.13.39) (EC-NOS) (NOS, TYPE III) (NOSIII) (ENDOTHELIAL NOS) (CONSTITUTIVE NOS) (CNOS).
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TISSUE-Aortic endothelium;
MEDLINE-92348367; Pubmed-1379225;
Sessa W.C., Harrison J.K., Barber C.M., Zeng D., Durieux M.E.,
D'Angelo D.D., Lynch K.R., Peach M.J.;
"Molecular cloning and expression of a cDNA encoding endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96102197; PubMed-8524847;
Roblinson L.J., Michel T.;
"Mutagenesis of palmitoylation sites in endothelial nitric oxide synthase identifies a novel motif for dual acylation and subcellular
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93055455; PubMed-1385480; Nishida K., Harrison D.G., Navas J.P., Fisher A.A., Dockery S.P., Ulmartsu M., Nerem R.M., Alexander R.W., Murphy T.J.; Molecular cloning and characterization of the constitutive bovine a
                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Lamas S., Marsden P.A., Li G.K., Tempst P., Michel T.;
"Endothelial nitric oxide synthase: molecular cloning and
characterization of a distinct constitutive enzyme isoform.";
Proc. Natl. Acad. Sci. U.S.A. 89:6348-6352(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Busconi L., Michel T.; "Endothelial nitric oxide synthase. N-terminal myristoylation determines subcellular localization.";
J. Biol. Chem. 268:8410-8413(1993).
                                                                                                                      DB 1; Length 1202;
ZINC.
ZINC.
E -> D (IN CORONARY SPASM).
FITIGHAR_008037.
S -> R (IN REF. 8).
G -> S (IN REF. 9).
V -> W (IN REF. 5).
V -> W (IN REF. 7).
D -> E (IN REF. 6).
MW; 93D127D6C14AC92E CRC64;
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Pred. No.
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52.9%;
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                                                                                                                                         Conservative
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488
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Matches 9; Conserv
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                                                                            REMOURS 393131, Table 39131, Kral V., Masters B.S., Poulos T.L.;
"Crystal structure of constitutive endothelial nitric oxide synthase:
"Crystal structure of constitutive endothelial nitric oxide synthase:
a paradigm for pterin function involving a novel metal center.";
Call 95:939-950(1998).

-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A CGMP-MEDIATED SIGNAL TRANSDUCTION PATHMAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) INDUCED ANGIOGENESIS IN CORONARY VESSELS AND PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS.
-!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) - CITRULLINE + NITRIC OXIDE + N NADP(+).
-!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FWN. ALSO REQUIRES
                                                                                                                                                                                                                                                                                                                                                          TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
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S -> Y (IN REF. 3).

T -> P (IN REF. 3).

T -> A (IN REF. 3).
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FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
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PRINTS; PR00371; FPNCR.
Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;
Lipoprotein; Palmitate; Phosphorylation; Calcium-binding; Heme;
Zinc; Metal-binding; Multigene family; 3D-structure.
INIT MET
                                                                                                                                                                                                                                                                                                                                                                                                      -! - ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY CAPK).
Proc. Natl. Acad. Sci. U.S.A. 92:11776-11780(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> SA (IN REF. 3).
-> V (IN REF. 3).
-> LV (IN PET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V (IN REF. 3).
                                         X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 66-481.
MEDLINE=99091052; PubMed=9875848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C -> R (IN REF.
Y -> I (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYRISTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PALMITATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PALMITATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZINC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L
WF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003097; -.
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M99057; AAA30667.1; -.
EMBL; M89952; AAA30494.1; -.
EMBL; M95674; AAA30669.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB; 1NSE; 18-MAY-99.
PDB; 2NSE; 25-MAY-99.
PDB; 4NSE; 18-MAY-99.
PDB; 4NSE; 18-MAY-99.
InterPro; 1PR001094; ...
InterPro; IPR001433; ...
InterPro; IPR001709; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511
681
805
946
1124
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803
856
906
1041
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491
650
794
936
1011
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25
25
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142
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317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation vpdate)
GENOME POLYPROTEIN (CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
P2A TO P2C, P3A; GENOME-LINKED PROTEIN VPG; PICORNAIN 3C
(EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D
(EC 2.7.7.48)].
                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Cardiovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-84169586; PubMed-6324136; MEDLINE-84169586; PubMed-6324136; Palmenberg A.C., Kirby E.M., Janda M.R., Drake N.L., Duke G.M., Potratz K.F., Collett M.S.; This polyprotein coding region."; The nucleotide and deduced amino acid sequences of the encephalomyocarditis viral polyprotein coding region."; Nucleic Acids Res. 12.2969-2985(1984) a A PROTEASE THAT CLEAVES AT CERTAIN Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.

1. FUNCTION: P3C POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.

C/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.

EACH OF WHICH IS COMPOSED OF ONE COPY BACH OF PROTEINS VP1, VP2, VP3, AND VP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polyprotein; Coat protein; Core protein; Transferase;
RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate.
1 67 LEADER PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENOME-LINKED PROTEIN VPG (H).
PICORNAIN 3C (P22).
RNA-DIRECTED RNA POLYMERASE P3D (E).
MRYRISTATE (BY SIMILARITY).
PROTEASE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEASE (POTENTIAL).
W; 26BC81BB7CF68CB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COAT PROTEIN VP4 (RHO).
COAT PROTEIN VP2 (BETA).
COAT PROTEIN VP3 (GAMMA
COAT PROTEIN VP1 (ALPHA
CORE PROTEIN P2A (G).
CORE PROTEIN P2B (I).
CORE PROTEIN P2B (I).
                                                                                                                                              PRT; 2290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00680; RNA_dep_RNA_pol; 1.
Pfam; PF00910; RNA_helicase; 1.
Pfam; PF00073; rhv; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255756 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X00463; CAA25152.1; -. PIR; A03906; GNNYE. HSSP; P12296; 1MEC.
                                                                                                                                                                                                                                                                                                                              Encephalomyocarditis virus
                         2 ALVQGILERVVDGPTP 17
                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000605; -. InterPro; IPR001205; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001676; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1802
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1606 162
1626 183
1831 229
68 1784 178
1802 180
2290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; C03.009; -.
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-12104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193
                                                                                                                                              POLG_EMCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIPID
                                                                                                        RESULT 11
                                                                                                                       POLG_EMCV
ID POLG
                                       q
                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-RD, KW20, ATCC 51907;
STRAIN-RD, KW20, KW20, ATCC 51907;
Fleischmann R.D., Adams W.D., White O., Clayton R.A., Kirkness E.F.,
Fleischmann R.D., Adams W.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback Tr., Hannam M.C., Nguyan D.T., Sauddek D.M., Brandon R.C.,
Grehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 269:496-512(1995).
-1- SUBUNIT: THOUGHT TO BE AN ATPASE SUBUNIT OF AN INTRACELLULAR ATP-DEPENDENT PROTEASE (BY SIMILARITY).
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0
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                              Length 1204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.4%; Score 46; DB 1; Length 856;
43.8%; Pred. No. 7.7;
ive 6; Mismatches 3; Indels
                                                                                                      6; Indels
  D017210062ABE4B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95837 MW; B8958ED9BD03EA3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-DEPENDENT PROTEASE (BY SIMILARITY).
                                                              ij
                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CLPB PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (POTENTIAL).
                                                            DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                      Mismatches
                                                            Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; 19039; 1.
Pfam; PF00495; clpA_B; 1.
PRINTS; PR00300; CLPPROTEASEA.
PROSITE; PS00870; CLPAB_1; 1.
PROSITE; PS00871; CLPAB_2; 1.
Chaperone; ATP-binding; Repeat.
DOMAIN 161
  133155 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U32767; AAC22518.1; -.
                                                            49.5%;
52.9%;
                                                                                                                                                                     808 PGLVEALLSRVEDPPPP 824
                                                        Query Match 49.5
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                          1 PALVOGILERVVDGPTP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     722
213
612
                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae.
1204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P21346; 1GRJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               856 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID: 727;
                                                                                                                                                                                                                                                                                                                                                                                                          CLPB OR HI0859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR; HI0859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus
                                                                                                                                                                                                                                                                                    CLPB_HAEIN
P44403;
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
SEQUENCE
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RESULT 10
CLPB_HABIN
ID P4440_3H
AC P4440_3H
DT 01-NOV
D

(BETA). (GAMMA). (ALPHA)

DOMAIN

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CHAIN
LIPID
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
CHAIN
CHAIN
                                                                                                                                                                                                                                                                              POLG_EMCVD
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 FFFS
                                                                                                                                                                                                            g
                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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REMBL; M2497, CONTENTS.

RESSP, P12296; 1MEC.

DR MEROPS; C03.009; --

DR MEROPS; U39.001; --

DR InterPro; IPR001205; --

DR InterPro; IPR001505; --

DR Pfam; PF00680; RNA_dep_RNA_pol; 1.

DR Pfam; PF000703; rNA' 3.

RW Polyprotein; Coat protein; Transferase; Myristate.

KW RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate.

Thomas Pfam; Pf00073; Mymerase; Hydrolase; Thiol protease; Myristate.

The polyprotein; Coat protein; Core protein; Transferase; Myristate.

The process of the protein of the pr
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variants of encephalomyocarditis virus.";

Virology 170:282-287(1989).

-!- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.

-!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS, EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VP3, AND VP4.
-!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89243189; PubMed=2541543;
Bae Y.S., Eun H.M., Yoon J.W.;
"Genomic differences between the diabetogenic and nondiabetogenic
                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COAT PROTEIN VP4 (RHO).
COAT PROTEIN VP2 (BETA).
COAT PROTEIN VP3 (GAMMA).
COAT PROTEIN VP3 (GLPHA).
CORE PROTEIN P2A (G).
CORE PROTEIN P2B (I).
CORE PROTEIN P3C (F).
CORE PROTEIN P3A.
GENOME-LINKED PROTEIN VPG (H).
PICORNAIN 3C (P22).
                              DB 1; Length 2290;
                                                              4; Indels
                                                                                                                                                                                                             PRT; 2292 AA
                                                              1; Mismatches
                              Score 46;
Pred. No.
                              48.48;
                                                              Conservative
                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137
393
624
901
1058
1194
1519
1607
1627
                                                                                           5 QGILERVVDGPTPH 18
               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=12105;
                                                                                                                                                                                                                                                                                                                                                                                            Cardiovirus
                                                                                                                                                                                                             POLG_EMCVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                           POLG_EMCVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1990 (Rel. 15, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
P2A TO P2C, P3A; GENOME-LINKED PROTEIN VPG; PICORNAIN 3C
(EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Encephalomyocarditis virus (strain emc-d diabetogenic).
Viruses: ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VP3, AND VP4.
-!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variants of encephalomyocarditis virus.";

Virology 170:280-287(1989).

-!- FUNCTION: P3C POLYPEPTIDE A PROTEASE THAT CLEAVES AT CERTAIN

Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.

-!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,

EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polyprotein; Coat protein; Core protein; Transferase;
RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate.
PROPEP 1 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDILNE-89243189; Pubmed-2541543;
Bae Y.S., Eun H.M., Yoon J.W.;
"Genomic differences between the diabetogenic and nondiabetogenic
RNA-DIRECTED RNA POLYMERASE P3D (E).
MYRISTATE (BY SIMILARITY).
PROTEASE (POTENTIAL).
PROTEASE (POTENTIAL).
MY. 8540D0E81437E8D4 CRC64;
                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                 Score 46; DB 1; Length 2292;
Pred. No. 22;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COAT PROTEIN VP4 (RHO).
COAT PROTEIN VP2 (BETA).
COAT PROTEIN VP3 (GAMMA).
COAT PROTEIN VP1 (ALPHA).
CORE PROTEIN P2A (G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2292 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000605; -.
InterPro; IRR001205; -.
InterPro; IPR001676; -.
Pfam, PF00680; RNA_dep_RNA_pol; 1.
Pfam; PF00910; RNA_helicase; 1.
Pfam; PF00073; rhv; 3.
                                                                                                                                                                                                       48.48;
64.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M22458; AAA43034.1; -. PIR; A31473; GNNYED.
                                                                                                                255495
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
     2292
68
1786
                                                                                      1804
                                                                                                                                                                                                                                                                                                                  5 QGILERVVDGPTPH 18
                                                                                      1804 180
2292 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P12296; 1MEC.
MEROPS; C03.009; -.
MEROPS; U29.001; -.
                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=12106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLG_EMCVD
P17594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cardiovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-9825987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Elgimeier K., Gas S., Barry C.E. III, Takaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Deviln K., Feltwell T., Gentles S., Hamin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,
Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                               011148.
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
ACETYLMURAMATE DEHYDROGENASE).
MURB OR RV0482 OR MTCY20G9.08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptidoglycan synthesis; Cell wall; Cell division; Oxidoreductase;
NADP; Flavoprotein; FAD.
SEQUENCE 369 AA; 38521 MW; 50AC021602ED9822 CRC64;
                             CORE PROTEIN P3A.
GENOME-LINKED PROTEIN VPG (H).
PICORNAIN 3C (P22).
RNA-DIRECTED RNA POLYMERASE P3D (E).
                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: UDP-N-ACETYLMURAMATE + NADP(+) =
UDP-N-ACETYL-3-O-(1-CARBOXYVINYL)-D-GLUCOSAMINE + NADPH.
-i- COFACTOR: FAD (BY SIMILARITY).
-i- PATHMAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-i- SUBLERILY: BELONGS TO THE MURB FAMILY.
                                                                                                                                                                                                  Score 46; DB 1; Length 2292;
                                                                                                                                                                                                                                   4; Indels
                                                                                                                                 PROTEASE (POTENTIAL).
                                                                                                MYRISTATE (BY SIMILARITY). PROTEASE (POTENTIAL).
               (F)
PROTEIN P2B (I)
PROTEIN P2C (F)
                                                                                                                                                                                                                                                                                                                                                                                     369 AA
                                                                                                                                                                                                                Pred. No. 22;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
               CORE
                                                                                                                                                                                                  48.48;
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                                                                                                                                                AA; 255426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                Query Match
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TubercuList; Rv0482; -.
               1519
1607
1627
1832
2292
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1786
1804
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                                                1608
1628
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1786
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ACT_SITE
SEQUENCE
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Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Horluchi T., Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai H., Kashimoto K., Kim S., Kimara S., Kitagawa M., Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Mashimoto H., Mishio Y., Oshima T., Salito N., Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91294165; PubMed-1906060;
Kitagawa M., Wada C., Yoshloka S., Yura T.;
"Expression of ClpB, an analog of the ATP-dependent protease
regulatory subunit in Escherichia coli, is controlled by a heat shock
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90239044; PubMed-2185473;
Gottesman S., Squires C., Pichersky E., Carrington M., Hobbs M., Mattick J.S., Dalrymple B., Kuramitsu H., Shiroza T., Foster T., Clark W.P., Ross B., Squires C.L., Maurili M.R.;
Clark W.P., Ross B., Squires C.L., Maurili M.R.;
"Conservation of the regulatory subunit for the Clp ATP-dependent protease in prokaryotes and eukaryotes.";
Proc. Natl. Acad. Sci. U.S.A. 87:3513-3517(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 753-857 FROM N.A.
BEDLINE-82247208; Pubmed-6255294;
Shen W.-F., Squires C.L.;
"Nucleotide sequence of the rrnG ribosomal RNA promoter region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                         7;
                             Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                            Indels
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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                            .
9
                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CLPB PROTEIN (HEAT SHOCK PROTEIN F84.1).
47.9%; Scor.
36.0%; Pred. No. 3...
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  857 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 10:3303-3313(1982)
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                      262 PVVTQDVYERLAGDAATRKDGPVPH 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sigma factor (sigma 32).";
J. Bacteriol. 173:4247-4253(1991).
                                                                                                                                                    1 PALVQGILERVV-----DGPTPH 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-31 FROM N.A.
STRAINHK12 / W3110;
                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia
                                                                                                                                                                                                                                                                                                                                                                              CLPB_ECOLI
P03815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN K12
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                       Query Match
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CLPB_ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001270; -.
Pfam; PFR0457; clpA=B; 1.
PRINTS; PR040300; CLPPROTEASEA.
PROSITE; PS00870; CLPAB=1; 1.
PROSITE; PS00871; CLPAB=2; 1.
Chaperone; AFP-binding; Repeat; Heat shock; Alternative initiation.
CHAIN 1857
                                                                                                          Pontis E., Sun X.Y., Joernvall H., Krook M., Reichard P., "ClpB proteins copurify with the anaerobic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.4%; Score 45; DB 1; Length 857; 37.5%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KL -> NV (IN REF. 1).
L -> V (IN REF. 1).
FD38CD96B2F7C32A CRC64;
                                                                Biochem. Biophys. Res. Commun. 180:1222-1226(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLPB PROTEIN.
CLPB PROTEIN 3.
FOR CLPB PROTEIN 3.
          SEQUENCE OF 1-14; 150-157; 355-364 AND 452-460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I.
II.
ATP (POTENTIAL).
ATP (POTENTIAL).
                                                                                       IDENTIFICATION AS A HEAT SHOCK PROTEIN.
                      MEDLINE-92062147; PubMed-1953774;
                                                                                                                                                                                                                                                                                                  MEDLINE-91294166; PubMed-2066329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MM.
                                                                                                                                                                                                                                                                                              EMBL; M29364; AAA24422.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 37.5
Matches 6; Conservative
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409
722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
857 AA;
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CONFLICT
CONFLICT
SEQUENCE
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DOMAIN
NP_BIND
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2 ALVQGILERVVDGPTP 17

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Gaps

0;

Indels

Mismatches

Search completed: September 10, 2001, 14:09:53 Job time: 562 sec

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Compugen Ltd
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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OM protein - protein search, using sw model

; Search time 42.28 Seconds
(without alignments)
32.430 Million cell updates/sec September 10, 2001, 14:01:14 Run on:

1 PALVQGILERVVDGPTPH 18 US-08-833-506C-30 95 Perfect score: Sednence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed 80 Minimum

Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ATP-dependent Cip ATP-binding protei endopeptidase Cip, endopoptidase Cip, CipB protein NMA16 CipB protein NMA16 nitric-oxide synth itric-oxide synth probable Tub famil ATP-dependent prot clp proteinase ATP nitric-oxide synth capsid polyprotein capsid polyprotein probable murB prot nitric-oxide synth probable phosphoes genome polyprotein nitric-oxide synth polyprotein polyprotein ATP-dependent Clp Description genome SUMMARIES 156575 JC5028 JC5029 D75500 B83319 H72258 F64098 GNNYE GNNYED GNNYEB A43271 S47647 S38253 I53165 F81078 D82814 25027 F69823 E84562 E86694 T34902 865440 A49676 A38943 :81863 1 DB Query Match Length 22292 2292 2292 2292 369 662.1 662.1 662.1 577.9 577.9 577.9 644.9 649.5 7 Score Result Š.

ATP-dependent prot ClpB protein PA454	endopeptidase Clp heat shock protein	<pre>b.3-phosphogiycera heat shock protein probable two-compo</pre>	conserved hypothet conserved hypothet probable secreted	sarcosine oxidase, probable hexosyltr	hypothetical ABC t hypothetical prote	cytoskeletal prote endopeptidase Clp,	probable endopepti
B86705 D83077	D35905 E85905	A/0464 F96771 B83055	E83102 T36841	F75144 A69989	C65129 H85999	S24609 H72404	C70834
0.0	- 77	900	0 0	7	0 0	0 0	7
816 854	857	911 911 983	322	379 407	637	651 820	848
47.4	47.4	4 4 4 6 6 . 3	45.3	45.3	45.3	45.3	45.3
45 45	45	7	4 4	43 83	43	43	43
30 31	33	3 3 4 5 5 4	320	39	41 42	43 44	45

ALIGNMENTS

		inc		16.	3893
		14.13.39),	_	revision.	G01947; I
		nitric-oxide synthase (EC 1.14.13.39),	Homo sapiens (man)	e #sedneuce	C; Accession: A49676; JX0345; G01947; I3893
1		xide synt	s: Homo sa	C; Date: 16-Feb-1996	ion: A4967
RESULT	A49676	nitric-o	C; Species:	C; Date:	C; Access

nitric-oxide synthase (EC 1.14.13.39), inducible - human C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Date: 16-Feb-1996 #text_change 20-Jun-2000
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 20-Jun-2000
C;Accession: A49676; Jx0345; G01947; I38933; S47566; A47475
R;Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; Hall, V.S.; Proc. Natl. Acad. Sci. U.S.A. 90, 11419-11423, 1993
A;Title: Cloning, characterization, and expression of a cDNA encoding an inducible ni A;Reference number: A49676; MUID:94068614

A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-1153 <RES.
A; Residues: 1-1153 <RES.
A; Cross-references: EMBL:X73029; NID:g441452; PIDN:CAA51512.1; PID:g441453
A; Cross-references: EMBL:X73029; NID:g441452; PIDN:CAA51512.1; PID:g441453
B; Hokari, A.; Zeniya, M.; Esumi, H.
J. Blochem. 116, 575-581, 1994
A; Title: Cloning and functional expression of human inducible nitric oxide synthase (A; Reference number: JX0345; MUID:95155267
A; Accession: JX0345

A; Accession: A079, L', 609-1153 < HOK>
A; Residues: 1-677, L', 609-1153 < HOK Band Cell line A-172
B; Park, C.; Park, R.; Krishna, G.
Submitted to the EMBL Data Library, July 1995
A; Reference number: 608912
A; Accession: 601947
A; Accession: 601947
A; Accession: 601947
A; References: EMBL: 01153 < PAR>
A; Residues: 1-607, L', 609-1153 < PAR>
A; Reference number: 138933; MUD: 95372368
A; Accession: 138933
A; Reference number: 138933; MUD: 955372368
A; Residues: 1-675, L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, 'L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, 'L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, 'L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, 'L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, 'L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, 'L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, 'L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, 'L', 677-932, 'G', 934-965, 'A', 967-1153 < RES
A; Residues: 1-675, 'L', 677-932

A; Reference number: S47566; MUID:94368816 A; Accession: S47566

A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-22, G', 24-153, 'L', 155-176, 'V', 178-799, 'A', 801-912, 'P', 914-1153 < MAI>
A; Cross-references: EMBL: U05810; NID: 9452487; PIDN: AAA56666.1; PID: 9452488
B; Geller, D.A.; Lowenstein, C.J.; Shapiro, R.A.; Nussler, A.K.; Di Silvio, M.; Wang, Proc. Natl. Acad. Sci. U.S.A. 90, 3491-3495, 1993

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A; Reference number: A46186; MUID:92357701
A; Accession: A46186
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81.2%;
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94.1%;
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Matches 16; Conservative
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Matches 13; Conserv
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A;Accession: A47475
A;Accession: A47476
A;Accession: A47476
A;Accession: A47476
A;Accession: A47476
A;Accession: A47476
A;Accession: A67476
A;Accession: A67476
A;Accession: A67476
A;Accession: A67476
A;Accession: A67476
A;Accession: A67477
A;Accession: A67
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Best Local Similarity
Matches 18; Conserv
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A Gene: NOS

C; Function:
A; Gene: NOS

C; Function:
A; Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NAD
A; Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NAD
C; Superfamily: nitric-oxide synthase; flavodoxin homology: NADPH--ferrihemoprotein re
C; Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FNN; heme; iron; me
F; 533-1121/Domain: flavodoxin homology <FEH>
F; 535-671/Domain: flavodoxin homology <FEH>
F; 194/Binding site: heme iron (Cys) (axial ligand) #status predicted
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Jun-2000
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Jun-2000
C;Accession: 347647; JC1472
Biochim. Biophys. Acta 1218, 421-424, 1994
A;Title: cDNA Acta 1218, 421-424, 1994
A;Title: cDNA Acloning and expression of inducible nitric oxide synthase from rat vasc A;Reference number: S47647; MUID:94325351
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A; Residues: 1-1147 < GCBN>
A; Cross-references: EMBL: 776881; NID:g439283; PIDN:CAA54208.1; PID:g439284
A; Cross-references: EMBL: 776881; NID:g439283; PIDN:CAA54208.1; PID:g439284
B; Nunokawa, Y:; Ishida, N:; Tanaka, S.
Biochem. Biophys. Res. Commun. 191, 89-94, 1993
A; Title: Cloning of Inducible nitric oxide synthase in rat vascular smooth muscle of A; Reference number: JC1472; MUID:93191721
A; Reference number: JC1472; MUID:93191721
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nitric-oxide synthase (EC 1.14.13.39) - rat
C;Species: Rattus norveglcus (Norway rat)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Jun-2000
C;Accession: $38253; JN0457
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A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
A;Rossidues: 1-190, 'V', 192-765, 'P', 767-843, 'G', 845-1144 <LOW>
A;Cross-references: GB:M92649; NID:9200109
A;Experimental source: BALB/C, RAW 264.7 cells, macrophage
A;Note: sequence extracted from NCBI backbone (NCBIP:113541)
C;Genetics:
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Pred. No. 0.2;
1; Mismatches
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A. Molecule type: mRNA
A. Residues: 1-1147 (~TSO)
A. Cross-references: DBJ:DBJ661; NID:g1209382; PIDN:BAA12035.1; PID:g1853973
A. Cross-references: DBJ:DBJ:DBJ661; NID:g1209382; PIDN:BAA12035.1; PID:g1853973
A. Experimental source: Kidney
C. Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein re
C. Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; fron; me
F.191-199/Domain: heme-binding #status predicted <HMB>
F.536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>
F.536-714/Domain: flavodoxin homology <FLX>
F.536-674/Domain: flavodoxin homology <FLX>
                                                                                       nitric-oxide synthase (EC 1.14.13.39) K - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 20-Jun-2000
C;Accession: JC5027
R;Tsutsumishita, Y:; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa Biol. Pharm. Bull. 19, 1374-1376, 1996
A;Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, an A;Reference number: JC5027; MUID:97070590
A;Reference number: Gcdd sequence not shown
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 05.May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C;Accession: 156575
R;Galea, E.; Reis, D.J.; Feinstein, D.L.
J. Neurosci. Rss. 37, 406-444, 1994
J. Neurosci. Rss. 37, 406-444, 1994
A;Title: Cloning and expression of inducible nitric oxide synthase from rat astrocyte
A;Reference number: 156575; MUID:94231594
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A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1147 <RRS>
A; Cross-references: EMBL:U03699; NID:9430718; PIDN:AAC13747.1; PID:9430719
C; Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein: C; Seyvords: calmodulin binding: chromoprotein; FAD; flavoprotein; FMN; heme; Iron; IF F; 536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>
F; 538-674/Domain: lavodoxin homology <FLX>
F; 538-674/Domain: flavodoxin homology <FLX>
F; 547/Finding site: heme iron (Cys) (axial ligand) #status predicted
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nitric-oxide synthase (EC 1.14.13.39) L - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 04-Mar-2000
C;Accession: JC5028
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F;764-775,899-910/Domain: FAD binding #status predicted <FAD>
F;975-993,1054-1067/Domain: NADP binding #status predicted <NDP>
F;975-993,1054-1067/Domain: NADP binding #status predicted <NDP>
F;977-81nding site: heme iron (Cys) (axial ligand) #status predicted
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Pred. No. 0.91;
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Pred. No. 0.2;
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80.0%;
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81.2%;
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Matches 12; Conservative
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Matches 13; Conser
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                                                                                                                                                                     A Accession: 338253
A; Molecule type: mRNA
A; Restraction: 1147 (Ann.)
A; Recession: 338253
A; Molecule type: mRNA
A; Restraction: 1147 (Ann.)
A; Experimental source: 11ver
B; Wood, E.R.; Berger Ur., H; Sherman, P.A.; Lapetina, E.G.
B; Rochem. Blophys. Res. Commun. 191, 767-774, 1993
A; Fitle: Hepatocytes and macrophages express an identical cytokine inducible nitric oxid
A; Reference number: JN0457; MUID:93221515
A; Recession: JN0457; MUID:93221515
A; Residues: 1-41, SS, 44-103, 105-190, Q, 192-213, R, 215-247, T, 249-263, I, 265-373, IE
S; Residues: 1-41, SS, 44-103, 105-106, EQ', 1029-1147 <WOO>
A; Cross-references: PIDN:AAB26037.1
A; Experimental source: liver
C; Genetics:
C; Genetics:
C; Genetics:
C; Circustion: A; Contribution: Contribution: A; Contribution: Cont
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 153165
R;Karlsen, A.E.; Andersen, H.U.; Vissing, H.; Larsen, P.M.; Fey, S.J.; Cuartero, B.G.; R;Karlsen, A.E.; Andersen, H.U.; Vissing, H.; Larsen, P.M.; Fey, S.J.; Cuartero, B.G.; R;Tile: Cloning and expression of cytokine-inducible nitric oxide synthase cDNA from rath A;Reference number: 153165; MUID:95309542
A;Tile: Cloning and expression of cytokine-inducible nitric oxide synthase cDNA from rath A;Reference number: 153165
A;Accession: 153165
A;Accession: 153165
A;Residues: 1-1147 <RES>
A;Residues: 1-1147 <RES>
A;Residues: 1-1147 <RES>
C;Genetics:
A;Genetics:
A;Gen
         Kawasaki, H.;
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A;Title: Molecular cloning of a cDNA encoding an inducible calmodulin-dependent nitric-A;Reference number: S38253; MUID:94039059
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Pred. No. 0.2;
1; Mismatches 2; Indels
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0.2;
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Pred. No. 0.2;
1; Mismatches
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Best Local Similarity 81.2%;
Matches 13; Conservative
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81.2%;
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Best Local Similarity 81.2
Matches 13; Conservative
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Length 1147;

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Probable phosphoesterase (EC 3.1.-.-) yhcR - Bacillus subtilis

N;Alternate names: 5-nucleotidase homolog yhcR
C;Species: Bacillus subtilis
C;Species: Bacillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Berr
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasamoto, K.; Yata, K.; Yoshida
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A;Reference number: Asobson: Roban.
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Cross-references: GB:299108; GB:AL009126; NID:92633055; PIDN:CAB12747.1; PID:e11829
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C.Comment: This sequence has motifs characteristic of a variety of phosphoesterases
          chromoprotein; FAD; flavoprotein; FMN; heme; iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: unassigned probable phosphoesterases; phosphoesterase core homology
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nitrito-oxide synthase (EC 1.14.13.39), endothelial - human
C.Species: Homo sapiens (man)
C.Spate: 02-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 03-Mar-2000
                                                                                                       F;336-1124/Domain: NADPH--ferrihomoprotein reductase homology <FEH>F;538-674/Domain: flavodoxin homology <FLX>F;538-674/Domain: flavodoxin homology <FLX>F;538-674/Region: biopterin binding predicted F;620-647/Region: FMN binding #status predicted F;764-775/Region: FAD binding #status predicted F;961-993/Region: RAD binding #status predicted F;975-993/Region: NADPH binding #status predicted F;1074-1087/Region: NADPH Binding Mstatus Pinding Mstatus
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Keywords: hydrolase
:591-682/Domain: phosphoesterase core homology <PEC>
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Pred. No. 0.91;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pro
                C;Keywords: calmodulin binding; chro
F;506-535/Region: calmodulin binding
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64.3%;
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Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity
Matches 9; Conserv
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C; Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 04-Mar-2000
C; Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 04-Mar-2000
C; Accession: 105029
R; Tautsumishita, Y:; Kawai, Y:; Rawai, Y:; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa, M. A; Tattesumishita, Y:; Rawai, Rawa
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S65440

intric-oxide synthase (EC 1.14.13.39) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
C;Accession: S65440
R;Twashina, M; Hirata, Y; Imai, T; Sato, K; Marumo, F.
Eur. J. Blochem. 237, 668-673, 1996
A;Title: Molecular cloning of endothelial, inducible nitric oxide synthase gene from rat
A;Reference number: S65440; MuID:96235231
A;Status: not compared with conceptual translation
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein redud
                                                Biol. Pharm. Bull. 19, 1374-1376, 1996
A; Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and uA; Reference number: JC5027; MUID:97070590
A; Reference number: JC5028
A; Accession: JC5028
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-1147 <TSU>
A; Experimental source: lung
C; Comment: This protein synthesizes nitric oxide from L-arginine.
C; Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reduc C; Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal F; 536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>
F; 536-174/Domain: naph--ferrihemoprotein reductase homology stell>
F; 538-674/Domain: flavodoxin homology <FLX>
F; 197/Binding site: heme iron (Cys) (axial ligand) #status predicted
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'Tsutsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, tol. Pharm. Bull. 19, 1374-1376, 1996
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80.0%; Pred. No. 0.91;
tive 1; Mismatches 2; Indels
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Best Local Similarity 80.0
Matches 12; Conservative
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probable Tub family protein [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C.Accession: E84562
R.Lin, X.: Kaul, S.: Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nacrman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487
A.Scatus: preliminary
A; Molecule type: DNA
A; Residues: 1-386 <STO>
                   F;491-509/Region: calmodulin binding #status predicted
F;520-1159/Domain: NADPH--ferrihemoprotein reductase homology <FEH>
F;520-1159/Domain: Inavodoxin homology <FEX>
F;521-703/Domain: flavodoxin homology <FEX>
F;521-804/Region: FMN binding #status predicted
F;791-804/Region: FAD-pyrophosphate binding #status predicted
F;791-804/Region: RAD-pyrophosphate binding #status predicted
F;1010-1028/Region: NADP-adenine binding #status predicted
F;100-1124/Region: NADP-adenine binding #status predicted
F;3/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Modified site: aspartic acid (Asn) #status predicted
F;3/Modified site: heme iron (Cys) (axial ligand) #status predicted
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A;Molecule type: DNA
A;Residues: 1.748 <STO>
A;Cross-references: GB:AE005176; NID:912723443; PIDN:AAK04655.1; GSPDB:GN00146
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Pred. No. 14;
2; Mismatches
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3; Mismatches
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A;Gene: At2g18280
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A; Note: this sequence has been revised in reference A49813
A; Cross-references: GB:M93718; NID:g189211
A; Note: this sequence has been revised in reference A49813
B; Garvey, E.P.; Tuttle, J.V.; Covington, K.; Merrill, B.M.; Wood, E.R.; Baylis, S.A.; Charch. Biochem. Biochem. Biophys. 311, 235-241, 1994
A; Title: Burification and characterization of the constitutive nitric oxide synthase from the session: S45691; MUID:94263196
A; Reference number: S45691; MUID:94263196
A; Rolecule type: protein
A; Residues: 'XX', 169-175; 531-536, 'X', 538-540; 835, 'X', 837-843, 'X', 845; 876-877, 'X', 879-881
A; Reperimental source: placenta
B; Nadaud, S.; Bonnardeaux, A.; Lathrop, M.; Soubrier, F.
B; Nadaud, S.; Bonnardeaux, A.; Lathrop, M.; Soubrier, F.
B; Nadaud, S.; Bonnardeaux, A.; Lathrop, M.; Soubrier, F.
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B; Nadaud, S.; Bonnardeaux, M.; Nadaud, S.; Nadaud, S.;
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A; Reference number: $24052; MUID:92354731
A; Reference number: $24052
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-1203 cARR2>
A; Cross-references: GB:M95296; NID:g189259; PIDN:AAA36372.1; PID:g189260
B; Janssens, S.P.; Shimouchi, A.; Quertermous, T.; Bloch, D.B.; Bloch, K.D.
A; Reference number: A38948
A; Reference number: A38948
A; Molecule type: mRNA
A; Residues: 1-1203 cARN1>
A; Residue
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A; Residues: 1-1203 <AMRI>>
A; Cross-references: GB:L10709; NID:G348235; PIDN:AAA36365.1; PID:G348237; GB:L10693; NID
0698; NID:G348224; GB:L10709; NID:G348225; GB:L10700; NID:G348226; GB:L10701; NID:G34822
DIG:G34823; GB:L10707; NID:G348233; GB:L10708; NID:G348234
R; Marsden, PA.; Schappert, K.T.; Chen, H.S.; Flowers, M.; Sundell, C.L.; Wilcox, J.N.;
FEBS Lett. 307, 287-293, 1992
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A;Introns: 53/2; 90/3; 140/2; 194/3; 225/2; 272/3; 319/2; 377/3; 411/3; 476/3; 501/2; 54
C;Function:
C;Accession: A47501; S24052; A38948; A49813; A42867; S45691; I37361
R;Marsden, P.A.; Heng, H.H.Q.; Scherer, S.W.; Stewart, R.J.; Hall, A.V.; Shi, X.M.; Tsui
J. Biol. Chem. 268, 17478-17488, 1993
A;Title: Structure and chromosomal localization of the human constitutive endothelial ni
A;Reference number: A47501; MUID:9335239
A;Accession: A47501
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A;Residues: 1-82,'S',84-179,'F',181-566,'W',568-647,'Q',649-854,'V',856-1008,'G',1010-11
PSQ','QRYPRAXCHPLPVS' <JAN3>
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A; Molecule type: mRNA
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A;Cross-references: GDB:209976; OMIM:163729
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Gaps

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clyptotednase ATP-binding chain - Streptomyces coelicolor
C; Species: T44902
R; Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
A; Caccession: T34902
A; Reference number: 221561
A; Accession: T34902
A; Stetus: preliminary; translated from GB/EMBL/DDBJ
B; Stetus: preliminary; translated fro
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          Score 47; DB 2; Length 748;
Pred. No. 12;
6; Mismatches 3; Indels
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49.5%; Score 47; DB 2; Length 842;
Best Local Similarity 43.8%; Pred. No. 14;
Matches 7; Conservative 5; Mismatches 4; Indels
               49.58;
Query Match
Best Local Similarity 43.8'
Matches 7; Conservative
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Search completed: September 10, 2001, 14:01:15 Job time: 214 sec

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2 ALVQGILERVVDGPTP 17

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12
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(without alignments)
16.268 Million cell updates/sec
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                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                            September 10, 2001, 14:00:24
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                           US-08-833-506C-30
95
1 PALVQGILERVVDGPTPH 18
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human iNOS peptide	Human iNOS (781-79	Human iNOS peptide	Inducible nitric o	Sequence encoded b	Nitric-oxide-synth	Hepatocyte inducib				
SUMMARIES	4	AAW81179	AAW81271	AAW81276	AAW81205	AAW81206	AAW81209	AAW96322	AAR55764	AAR63206	AAR88464
% Query Match Length DB	18 19	18 19	18 19	18 19	18 19	18 19		1146 20	1153 15	1153 15	1153 17
% Query Match L	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	95	95	95	95	95	95	95	95	95	95	95
Result No.	п	7	က	4	S	9	7	80	σ	10	11

Human inducible ni Amino acid sequenc Human inOs peptide Human iNOS peptide Mouse iNOS (776-79 Inducible nitrico Inducible nitrico Human iNOS peptide Human noos peptide Human noos peptide Human noos peptide Human noothelial Amino acid sequenc Human nitric oxide Bovine endothelial Staphylococcus aur Amino acid sequenc Human iNOS peptide Human iNOS peptide	human; immunoassay; detection; n; sepsis; septic shock; lupus; transplantation; psoriasis; dated"
AAM336113 AAB31724 AAM81233 AAW81233 AAW81234 AAW81237 AAW81237 AAW81237 AAW81237 AAW81237 AAW81239 AAW81238 AAW81238 AAW81238 AAW81238 AAW81238 AAW81238 AAW81238 AAW81238 AAW81233 AAW81233 AAW81233 AAW81233 AAW81333 AAW81333 AAW81333 AAW81333 AAW81333 AAW81333 AAW81333 AAW81333 AAW81333 AAW81333 AAW81333 AAW81333 AAW81333 AAW81333 AAW81333 AAW81333 AAW81333	A. A. Tinos; Titatio jection erosis. ers
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                                                                                                               This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (inOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inducible nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.
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             Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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Pred. No. 7.1e-10;
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                                                                                  Example 4; Page 36; 93pp; English.
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100.0%;
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Matches 18; Conservative
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tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple scherosis. This sequence represents a peptide fragment from human iNOS which is used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monoclonal antibody; mimic; mimic; mimic; mimicioassay; defection; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nitric oxide synthase; iNOS; human; immunoassay; detection;
                                                                                                                                                                                               Gaps
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                                                                                                                                                               Length 18;
                                                                                                                                                                                              Indels
                                                                                                                                                            100.0%; Score 95; DB 19;
100.0%; Pred. No. 7.1e-10;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Human iNOS peptide fragment PS-5166.
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Modified-site
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This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                               Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis; Mab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
                                                                                                                                         Human iNOS peptide fragment capable of binding Mab 2D2-B2.
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                     AA.
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                   AAW81205 standard; peptide; 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Webber R;
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                                                            AAW81205;
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AAW81205
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                                                                                                                                                                                                                                                                                                                                                                                                                                    detection;
ock; lupus;
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes an immunoassay method where a sample with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Inducible; nitric oxide synthase; iNOS; human; immunoassay; detectio monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupu myocardial infarction; tissue rejection; transplantation; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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                                        Length 18;
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0
                                      Score 95; DB 19;
Pred. No. 7.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 95; DB 19; 100.0%; Pred. No. 7.1e-10;
                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disease; multiple sclerosis.
                                                                                                                                                                                                                                                                 AAW81276 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 93pp; English.
                                    100.0%; Sc
100.0%; Pr
tive 0;
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                                                                                                                                                                                                                                                                                                                                                                                         Human iNOS peptide fragment #2.
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                                                                                                                                           1 PALVQGILERVVDGPTPH 18
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                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                      Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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es 18; Conserv
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WO9845710-A1

15-0CT-1998

Homo sapiens

myocardial

30-APR-1999

AAW81276;

AAW81276

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11-APR-1997; 07-APR-1997;

Webber R;

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Gaps

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Indels

Query Match Best Local S Matches 18

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Sequence

Length 18;

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specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (1NOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                             This invention describes an immunoassay method where a sample with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manganese containing superoxide dismutase; MnSOD; IDDM; diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell; fatty acid; lipotoxic; cytotoxic; cytokine; osteoporosis; inflammatory disease; autoimmune disease; neurodegenerative disease.
                                                                                      Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human INOS or mimics.
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 95; DB 19;
100.0%; Pred. No. 7.1e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW96322 standard; Protein; 1146 AA.
                                                                                                                                                Example 3; Page 33; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inducible nitric oxide synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US15781.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PALVOGILERVVDGPTPH 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BETA-) BETAGENE INC.
(TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SA, Hohmeier H, Ko
a M, Shimabukurom,
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-153448/13.
                                                        WPI; 1998-594495/50
                                                                                                                                                                                                                                                                                                                                                         18 AA;
   (WEBB/) WEBBER R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAX08434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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30-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-1999.
                              Webber R;
                                                                                                                                                                                                                                                                                                                               invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW96322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohneda M,
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                     This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis; Mab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                              Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human 1NOS peptide fragment capable of binding Mab 22E3-2F5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 95; DB 19;
Pred. No. 7.1e-10;
Mismatches 0;
autoimmune disease; multiple sclerosis; Mab
                                                                                                                                                                                                                                                                                                                            Example 3; Page 32; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW81209 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                    WPI; 1998-594495/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                            (WEBB/) WEBBER R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 AA;
                              Homo sapiens
                                                        WO9845710-A1
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                                                                                                                   11-APR-1997;
                                                                                                                                              07-APR-1997;
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                                                                                       15-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                         Webber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Gaps

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Length 18; Indels

Protection of mammalian cells against immunotoxicity or lipotoxicity - used for treating, e.g. diabetes, obesity, wasting syndromes, Lee Y, Newgard CB; Unger RH Koyama K, Le , Thigpen A,

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                                                                                    achieved by blocking free radical puroduction or the accumulation of the radicals in that cell. Treatment of insulin dependent diabetes mellitus (IDDM) can be achieved by by blocking nitric oxide (NO) production in a pancreatic beta cell and by providing a composition comprising an agent that reduces levels of fatty acids in the cells and protects beta-cells of the subject against lipid-mediated cell ceath. Cells can also be protected against lipid-mediated cell cath. Cells can also be protected against litric oxide mediated cell cyctoxicity by introducing into the cell an antioxidising agent. The methods can be used for protecting cells against immunotoxicity mediated by, e. g. IL-1 beta, IL-1 alpha, gamma IFN, TNF alpha, TNF cells. IL-2, IL-6, IL-3, IL-5, IL-7, IL-9, IL-14, IL-17, granulocyte-macrophage colony stimulating factor or monocyte compostractant protein-1. The methods can be used for the treatment colong stimulating factor or monocyte mediated the protein-1. The methods can be used for the treatment of e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ66914 is from human hepatocyte inducible nitric oxide synthase clone pHINOS from lambda Zap II cDNA library. The original source was induced human hepatocyte RNA. HINOS cDNA plasmid is pref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoded by the cDNA clone for human hepatocyte inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA clone encoding human inducible nitric oxide synthase - used to prevent the hypotensive shock seen with sepsis.
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 95; DB 20; Length 1146; Pred. No. 8.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nitric oxide synthase; hepatocyte; hypotensive shock; therapy
                                                                                                                                                                                                                                                                                                         syndromes, short stature, osteoporosis, inflammatory s, autoimmune diseases, or neurodegenerative diseases.
                                                                           cells can
 or
osteoporosis, inflammatory diseases, autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                         Inhibition of cytokine mediated immunotoxicity of
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simmons RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                           Disclosure; Page 247-251; 253pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nussler AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR55764 standard; Protein; 1153 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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              neurodegenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PALVQGILERVVDGPTPH 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nitric oxide synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-200273/24.
                                                                                                                                                                                                                                                                                                                                                      1146 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-DEC-1994
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                                                                                                                                                                                                                                                                                                                           iseases,
                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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AAR55764
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transformed in E. coli SOLR (ATCC 69126). The inventors claim a clone with the CDNA sequence in AAQ66914 and a CDNA clone which encodes AAR55764. The cloning and expression of a human tissue nitric oxide synthase cDNA provides a source of the enzyme for therapeutic purposes, for example to prevent the hypotensive shock seen with sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nitric-oxide-synthase. cDNA was generated and used to construct a library in lambda ZAPII. This was screened with a 650 bp fragment of mouse inducible NO-synthase cDNA to identify the full-length clone PBSHSINOS. The insert was transferred to pSVL to give a vector capable of expressing NO-synthase in CHO cells under control of a
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human chondrocytes were incubated with interleukin-1-beta to induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor;
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                                                                                                                                                                                                                                                Length 1153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nitric-oxide-synthase; NO-synthase; NOS; chondrocyte; interleukin-1-beta; pBSHBINOS; arthritis, hypertension; septic shock; inflammation; ischemia; dementia; obesity; agonist; antagonist; vector; CHO; Chinese hamster ovary;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identifying enzyme inhibitors and stimulators, and and treatment of e.g. viral infections or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
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100.0%; Pred. No. 8.4e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                              Score 95; DB 15;
Pred. No. 8.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moncada
                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Charles IG, Moncada SE, Palmer RMJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 25-31; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heterologous constitutive promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR63206 standard; Protein; 1153
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                                                                                                                                                                                                                                              100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                   (WELL ) WELLCOME FOUND LTD.
                                                                                                                                                                                                                                                                                                                                        1 PALVQGILERVVDGPTPH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nitric-oxide-synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-333198/41.
                                                                                                                                                                         1153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1153 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ77700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-1994;
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(RAJF/) RAJFER J.
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   Homo sapiens
                                                       WO9742965-A1
                                                                                                                                                                            09-MAY-1997;
                                                                                                                                                                                                                                      10-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                 20-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An inducible nitric oxide syntase (iNOS - AAR88464) is the product of a cDNA clone (AAT10115) derived from human hepatocytes induced for iNOS blosynthesis. The iNOS can be obtd. by expression of the cDNA e.g. in mammalian host cells and is used in the development of selective inhibitors of NOS or to treat diseases affected by nitric oxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nitric oxide synthetase; NOS; iNOS; HPINOS; human; erectile dysfunction; impotence; gene therapy; corpora cavernosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inducible nitric oxide synthase gene - useful in gene therapy to treat, e.g. vascular occlusive disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                        Inducible nitric oxide synthase; iNOS; hepatocyte; gene therapy; vascular occlusive disease; cancer; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tzeng E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 95; DB 17;
Pred. No. 8.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                    Hepatocyte inducible nitric oxide synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 54-58; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nussler AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW36113 standard; Protein; 1153 AA.
                                                                                                                                                                                                    AAR88464 standard; Protein; 1153 AA.
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100.0%;
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                              781 palvqgilervvdgptph 798
PALVOGILERVVDGPTPH 18
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                                                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYPI-) UNIV PITTSBURGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-068641/07.
N-PSDB; AAT10115.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9600006-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JAN-1996
                                                                                                                                                                                                                                                                  AAR88464;
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                                                 셤
                                                                                                                                                                                                       NAME OF THE PROOF 
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This protein comprises human penis inducible nitric oxide synthetase (HPINOS). Its amino acid sequence was deduced from a contact cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of a human inducible nitric oxide synthase (NOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene therapy; angiogenesis; nucleic acid delivery; arteriosclerosis; nitric oxide synthase; NOS; endothelial dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment of erectile dysfunction - by introducing an agent into penile tissue, particularly for inducing cavernosal smooth muscle relaxation or increasing NOS levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 8.4e-08;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB31724 standard; Protein; 1153 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 38-41; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                               Rajfer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                      (GONZ/) GONZALEZ-CADAVID N F.
97WO-US07643
                                                                                                                   96US-0017373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUL-2000; 2000WO-NL00482.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Gonzalez-Cadavid NF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-008577/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1153 AA;
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us-08-833-506c-30.rag

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WPI; 1998-594495/50.
                                 1153 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (WEBB/) WEBBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                         WO9845710-A1
                                                                                                                                                                                                                            30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                               15-0CT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Webber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
                                                                                                                                                                                                        AAW81233;
                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                               RESULT 1
AAW81233
                                                                                                                                                                                                        QQ
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                                                                                                           δy
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                                                                                    Nucleic acid delivery vehicle comprising a nucleic acid encoding nitric oxide synthase, used for isolated tissue perfusion treatment to enhance
                                                                                                                                                The specification describes a method for gene therapy for enhancing and inducting angiogenesis. The method uses a nucleic acid delivery vehicle, which comprises a nucleic acid encoding nitric oxide synthase (NOS). The delivery vehicle is used for the manufacture of a pharmaceutical composition for isolated tissue perfusion treatment. The method is useful for enhancing and/or inducing angiogenesis in patients with endothelial dysfunctions, in particular arteriosclerosis. The present sequence represents an inducible NOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of a nucleic acid delivery vehicle comprising a nucleic acid encoding nitric oxide synthase, especially useful in gene therapy for enhancing and/or inducing angiogenesis and treating atherosclerosis \cdot
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to use of a nucleic acid delivery vehicle comprising a nucleic acid encoding nitric oxide synthase (NOS) activity for the manufacture of a composition for essentially isolated tissue perfusion treatment to enhance and/or induce
                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                  Length 1153;
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nitric oxide synthase; NOS; angiogenesis; gene therapy.
                                                                                                                                                                                                                                                                                Score 95; DB 22;
Pred. No. 8.4e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human inducible nitric oxide synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Examples; Page 14-18; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   AAB66724 standard; protein; 1153 AA
                                                                                                                              Disclosure; Fig 6; 37pp; English.
                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                100.0%;
100.0%;
99US-0143101.
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                                                                                                                                                                                                                                                                                                                          1 PALVQGILERVVDGPTPH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                          Vogels R, Verlinden SFF;
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                          and induce angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vogels R, Verlinden S;
                     (INTR-) INTROGENE BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INTR-) INTROGENE BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-125729/14.
                                                              WPI; 2001-123142/13.
                                                                                                                                                                                                                                                1153 AA;
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1067190-A1.
09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUL-1999;
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                                                                                                                                                                                                                                                  Seguence
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specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes an immunoassay method where a sample with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
anglogenesis. The nucleic acid delivery vehicle is particularly useful in gene therapy for the treatment of atherosclerosis.
                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                 Length 1153;
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                                                                                                                                                                                                              100.0%; Score 95; DB 22;
100.0%; Pred. No. 8.4e-08;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW81233 standard; peptide; 15 AA.
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100.0%;
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                                                                                                                                                                                                                 Query Match 100.

Best Local Similarity 100.
Matches 18; Conservative
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0; Gaps 0; Indels 0; Mismatches Matches 15; Conservative

0;

Qy Dp

Search completed: September 10, 2001, 14:00:25 Job time: 169 sec

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0987909 wuchereria
018479 meloidogyne
090x16 homo sapien
09hcc8 homo sapien
09rz18 deinococcus
09rx10 arabidopsis
091x80 arabidopsis
                                                 09p4el cunninghame
09pp6 drosophila
09na92 caenorhabdi
04663 corynabacte
09hg14 phanerochae
09hg2 phanerochae
09hdg2 phanerochae
09hdg2 bhanerochae
09kb53 bacillus ha
                                                                                                                                                                                                                                                                                                                                                                             09fp93 oryza sativ
060471 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9w1z6 drosophila
Q9sh73 arabidopsis
Q9uyq8 pyrococcus
                                                                                                                                                                       oryza sativ
                                                                                                                                                                                                                                                                                                                                                                                                  060471 homo sapien
Q9ubk8 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Ogawa Y., Nishijima S., Goto M., Ida M.;
Ogawa Y. Nishijima S., Goto M., Ida M.;
T "Cloning and characterization of a novel splice valiant of human
I "Cloning and characterization of a novel splice valiant of human
I inducible nitric oxide synthase.";
I submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL; AB022318; BAA37123.1; -.
R HSSP; P35228; 4NOS.
R InterPro; IPR001043; -.
R InterPro; IPR001709; -.
R InterPro; IPR001709; -.
R Ffam; PF00175; oxidored_fad; 1.
R Pfam; PF00667; FAL_binding; 1.
R PRINTS; PR00331; FAL_VENCRA, MAY. CIPO62A174435571 CRC64.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidee; Homo.
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                                     92dv6C
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larity 94.4%; Pred. No. 4.2e-07;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C1F9624774435571 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
INDUCIBLE NITRIC OXIDE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1114 AA
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Q9KB53
Q9YCT1
                                                                                                                                                                                                                           Q9XYU9
018479
Q9NXJ6
Q9HCC8
Q9RZI8
Q9HX6
Q9HX6
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060471
                                 09VP28
09P4E1
09GPP6
09NA92
046063
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
094994
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RESULT
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Q9tux8 canis famil
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Q9ttt6 oryctolagus
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Q9pu92 cyprinus ca
Q09590 caenorhabdi
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32.830 Million cell updates/sec
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                                                                                                                            September 10, 2001, 14:11:13; Search time 72.54 Seconds
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                                     Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                 GenCore version 4.5 Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                       425026 seqs, 132305027 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                          OM protein - protein search, using sw model
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Q9R0W4
Q9TTT6
Q9QW28
Q9PU92
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Q9JJY7
Q9N176
Q9TUX8
Q9WTK6
Q60451
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Q00141
Q16550
Q12181
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sp_vertebrate:*
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sp_mammal:*
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97
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sp_bacteria:*
sp_fungi:*
sp_human:*
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Maximum DB seq length: 2000000000
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sp_rodent:*
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Match Length DB
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Caprinae; Ovis.
                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
101-MAR-2001 (TrEMBLrel. 16, Last annotation update)
101-MAR-2001 (SATHASE.
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Mershon J.L., Clark K.E.; Mershon J.L., Clark K.E.; "Estrogen increases the expression of iNOS in the ovine coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 86; DB 6; Length 1154;
Pred. No. 4.6e-06;
2; Mismatches 1; Indels
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**InterPro: IPR001094; -...

**InterPro: IPR001094; -...

**InterPro: IPR001043; -...

**InterPro: IPR001709; -...

**InterPro: IPR001709; -...

**InterPro: IPR001709; -...

**InterPro: IPR001709; -...

**InterPro: IPR00179; -...

**InterPro: IPR00170; -...

**InterPro: IPR001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1154 AA; 131709 MW; 42CD606E447254CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INDUCIBLE NITRIC OXIDE SYNTHASE (FRAGMENT).
                     PRT; 1154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               945 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                  HSSP, P29477; 1NOS.
InterPro; IPR001094; -
InterPro; IPR001094; -
InterPro; IPR001039; -
InterPro; IPR001709; -
InterPro; IPR003097; -
Pfam; PF00175; oxidored_fad; 1.
Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1006 RMTLVFGCRRPDEDHLYR 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 88.7%;
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RMTLVFGSRRPDEDHIYQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                     PRELIMINARY;
                                                                                                                                                               Mammalia; Euther
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9N175
Q9N175;
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Q9N175
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RC STRAIN-WISTAR KYOTO;

RX MEDIATE-99326503; Pubbmed-10395902;

RX MEDIATE-99326503; Pubbmed-10395902;

RY MOLECULAR CLONING and characterization of the rat inducible nitric

RT Coxide synthase (INOS) gene.";

RMDIATE-99336503; Pubbmed-10395902;

RY Coxide synthase (INOS) gene.";

RMDIATE-9930463; CAB46089.1; JOINED.

BREAL, AJ230465; CAB46089.1; JOINED.

BREAL, AJ230465; CAB46089.1; JOINED.

BREAL, AJ230466; CAB46089.1; JOINED.

BREAL, AJ230470; CAB46089.1; JOINED.

BREAL, AJ230477; CAB46089.1; JOINED.

BREAL, AJ230480; CAB46089.1; JOINED.

BREAL, AJ230481; CAB46089.1; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID:10116;
                                                                                  Gaps
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       Length 945
                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1147 AA; 130613 MW; E76B3F8407D54CF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Score 81; DB 6; 1
Pred, No. 2.6e-05;
2; Mismatches 1,
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDUCIBLE NITRIC OXIDE SYNTHASE.
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Pfam: PF00667; FAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
   83.5%;
82.4%;
                                                                                                                                                                                               833 RMTLVFGCRRPEEDHLY 849
                                                                                                                                                    1 RMTLVFGSRRPDEDHIY 17
   Query Match 83.5
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001709; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003097;
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HSSP; P29477; 1N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9R0W4;
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InterPro; IPR003097; -. Pfam; PF00175; oxidored_fad; 1. Pfam; PF00667; FAD_binding; 1.
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                                                                                                                                                                                                                                    PRELIMINARY;
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Best Local Similarity
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01-NOV-1996 (
01-NOV-1996 (
01-OCT-2000 (
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE-93221515; PubMed-7682072; Wood B.R., Barger H.Jr., Sherman P.A., Lapetina E.G.; Hepatocytes and macrophages express an identical cytokine inducible nitric oxide synthase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                    Shi Y., Pritchard K.A., Baker J.E.; "Chronic myocardial hypoxia increases nitric oxide synthase and decreases caveolin-3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.3%; Score 74; DB 6; Length 82; 76.5%; Pred. No. 3e-05; 1ive 1; Mismatches 3; Indels
                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-NEW ZEALAND WHITE; TISSUE-KIDNEY;
TSAO L.S., O'Brien W.J.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                 82 AA; 9396 MW; 73244479A4B965F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYTOKINE INDUCIBLE NITRIC OXIDE SYNTHASE, INOS.
                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INDUCIBLE NITRIC OXIDE SYNTHASE NOS2 (FRAGMENT).
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-NEW ZEALAND WHITE; TISSUE-HEART MYOCARDIUM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 191:767-774(1993) HSSP; P29477; 1NOS.
                                                                               82 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1147 AA.
                                                                                                                                                                                                                                                                                                                                    Free Radic. Biol. Med. 29:695-703(2000).
EMBL: AF198443; AAF09500.1; -.
EMBL; AF200351; AAG24286.1; -.
                                                                               PRT;
            1006 RMTLVFGCRHPEEDHLYQ 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RMTLVFGSRRPDEDHIY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 RMILVFGCRHPDEDHLY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 76.5
Matches 13; Conservative
                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
 1 RMTLVFGSRRPDEDHIYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001094; -. InterPro; IPR001433; -. InterPro; IPR001709; -. InterPro; IPR002369; -.
                                                                                                                                                                                                                                                                                                                                                                        HSSP; P00388; 1AMO.
InterPro; IPR001709; -.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                     NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                          PubMed=11053770;
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NON_TER
SEQUENCE
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Q9QW28;
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Q9QW28
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A Saeij J.P., Stet R.J., Groeneveld A., Verburg-van Kemenade L.B.,
A Wiegertjes G.F.;
A Wiegertjes G.F.;
Indentification and characterization of a fish inducible nitric oxide
synthase CDNA.";
Indunogenetics 0.0-0(0).
I IRRUNOGENETICS CAB60197.1;
R HSSP; P29477; INOS.
R InterPro; IPR001094;
R InterPro; IPR001433;
R InterPro; IPR001439;
R InterPro; IPR001409;
R InterPro; IPR001009;
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Actinopterygil; Neopterygil; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
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                                                                                                                                                         70.1%; Score 68; DB 11; Length 1147; 72.2%; Pred. No. 0.0053;
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Pred. No. 0.58;
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                               2CAFB983E56F651A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INDUCIBLE NITRIC OXIDE SYNTHASE (EC 1.14.13.39).
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Last annotation update)
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PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1127 AA.
                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
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PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
PLODOM; PL001811; -; 1.
SEQUENCE 1147 AA; 130625 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00175; oxidored_fad; 1.
Pfam; PF00667; FAD_binding; 1.
PRIWTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyprinus carpio (Common carp)
                                                                                                                                                                                                                                                                                        ||||||| | |||||| 1006 RMTLVFGCRHRREDHLYQ 1023
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58.88;
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                                                                                                                                                                                                                                                             1 RMTLVFGSRRPDEDHIYQ 18
                                                                                                                                                      Query Match
Best Local Similarity 72.2'
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 MTLVFGSRRPDEDHIYQ 18
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EMBL; AB042615; BAA95684.1;
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                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                       Q9JJY7
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Q9N176
                                                                                                                                                                                                                                                              RESULT 10
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                                                                                                                                                                                                                                                            REDUCTAGE.

REDUCTAGE.

REDUCTAGE.

REDUCTAGE.

RESP. 101322; AAA62544.1; -.

RESP. 101322; AAA62544.1; -.

ROTHER POOL 10102.6; CE02018.

RICEPTO: IPR001094; -.

R InterPro: IPR001099; -.

R InterPro: IPR003099; -.

R Pfam; PF00175; oxidored_fad; 1.

R Pfam; PF00175; oxidored_fad; 1.

R PRINTS; PR00359; FLAVODXIN.

R PRINTS; PR00371; FPNCR.

W Hypothetical protein; Oxidoreductase; Flavoprotein; FMN; FAD; NADP;
                                                                                                                       Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5 (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME = NADP(+) + 2
FERROCYTOCHROME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horike N., Takemori H., Sonobe H., Nonaka Y., Okamoto M.;
"Molecular cloning of NADPH-cytochrome P450 reductase from silkworm
eggs and its involvement in biosynthesis of 20-hydroxyecdysone during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
NCBI_TaxID=7091;
                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                       FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
28271950576B0EE8 CRC64;
                                                                                                                                                                                                             (PROBABLE).
-!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME BS REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                  -1 - COFACTOR: THIS FLAVOPROTEIN BINDS ONE MOLE EACH OF FAD AND FMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
 PROBABLE NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 52; DB 5; Length 662;
Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the embryogenesis.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
NADPH CYTOCHROME P450 REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  687 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                               Endoplasmic reticulum; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75208 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.6%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | :| | | | |:| |:
545 MHLYYGCRHPDHDYIYK 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 MTLVFGSRRPDEDHIYQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 53.6
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bombyx mori (Silk moth)
                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                             NCBI_TaxID=6239;
                                                                                                               Miller N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NKV3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9NKV3
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                    Length 687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bachmann S., Bostanjoglo M., Nafz B., Oberbaeumer I.; "NO synthases in the kidney."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. InterPro; IPR01709; -. InterPro; IPR03097; -. InterPro; IPR03097; -. Pfam: PF00667; SAD_bhiding; 1. PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oberbaeumer I., Welp H., Bachmann S.;
"A cDNA probe for rat NOS3 for in situ hybridization.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6466628BF253EE13 CRC64;
                                                                                                                                                                    687 AA; 77688 MW; 57285830F159E0BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9JJY7;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ENDOTHELIAL NITRIC OXIDE SYNTHASE 3 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ENDOTHELIAL NITRIC OXIDE SYNTHASE (FRAGMENT).
                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                    Score 52; DB 5
Pred. No. 1.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 AA
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Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
      InterPro; IPR001433; ...
InterPro; IPR001433; ...
InterPro; IPR001009; ...
Pfam; PF000175; ox.4dored_fad; 1.
Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33803 MW;
                                                                                                                                                                                                                                      53.6%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.68;
58.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 MTLVFGCRCSQLDHLYR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 MTLVFGSRRPDEDHIYQ 18
                                                                                                                                                                                                                                 Query Match 53.6 Best Local Similarity 66.7 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                         4 LVFGSRRPDEDHIYQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306
InterPro; IPR001094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE-LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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us-08-833-506c-31.rspt

1206 AA.

PRT;

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1044 MTLVFGCRCSQLDHLYR 1060
                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         060451;
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                                                                                                                        Q9WTK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
Q60451
                                                                                RESULT 13
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                                                                                                     D9WTK6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
          Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mammalia; Eutheria; Cetartiodactyla; Ruminantla; Pecora; Bovoldea;
MCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schwemmer M., Bassenge E.; "Assembly and characterization of canine heart endothelial nitric oxide synthase cDNA and 5'-flanking sequence by homology (RT-)FCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                       SEQUENCE FROM N.A. Mershon J.L., Clark K.E.; "Estrogen increases the expression of iNOS in the ovine coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                  artery.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF223471; AAF34707.1;
InterPro; IPR001433;
InterPro; IPR001709;
InterPro; IPR003097;
InterPro; IPR003097;
InterPro; IPR001709;
InterPro; IPR001709;
InterPro; IPR001709;
InterPro; IPR001709;
InterPro; IPR001709;
InterPro; IPR00170;
IN
                                                                                                                                                                                                                                                                                                                                                                                                                                 794B274DA786A4A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.6%; Score 51; DB 6;
58.8%; Pred. No. 4.4;
iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 51; DB 6
Pred. No. 1.2;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99369487; PubMed=10442857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cloning.";

witric Oxide 3:254-264(1999).

EMBL; AF143503; AAD52161.1; -.

HSSP; P29474; 3NOS.

InterPro; IPR001094; -.

InterPro; IPR001433; -.

InterPro; IPR001709; -.

InterPro; IPR001709; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133045 MW;
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Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                               40791 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.6%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2000 (TrEMBLrel. 15, NITRIC OXIDE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 MTLVFGCRCSQLDHLYR 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 52.6
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 366 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
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Q9TUX8
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2 MTLVFGSRRPDEDHIYQ 18

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
NADPH-CYTOCHROME P450 OXIDOREDUCTASE.
Cricetulus griseus (Chinese hamstrer)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51; DB 11; Length 1206; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                               Derst C., Preisig-Mueller R., Rajan S., Daut J.;
"Cloning and sequencing of guinea pig NO synthases.";
Submitted (APR.1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF146040; AAD29753.1;
EMBL; AF146040; AAD29752.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1206 AA; 133692 MW; EB4E792D3F9503DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; D83230; BAA11856.1; -.
HSSP; P00388; 1AMO.
                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   667 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
      Created)
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01-NOV-1999 (TrEMBLrel. 12, Create U-NOV-1999) (TrEMBLrel. 12, Last s 01-MAR-2001) (TrEMBLrel. 16, Last ENDOTHELIAL NITRIC OXIDE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001094; -.
Interpro; IPR001433; -.
Interpro; IPR001709; -.
InterPro; IPR003097; -.
Pfam; PF00175; oxidored_fad; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00175; oxidored_fad; 1.
Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.6%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||| | ||:|:
1045 MTLVFGCRCSQLDHLYR 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 MTLVFGSRRPDEDHIYQ 18
                                                                                                                                                                                                                                                                                                                  HSSP; P29474; 3NOS.
InterPro; IPR001094; -.
InterPro; IPR001433; -.
InterPro; IPR001709; -.
InterPro; IPR001709; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-GOLDEN;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
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NCBI_TaxID=10029;
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"CDNA cloning and characterization of NADPH-cytochrome P-450 reductase
in human HL-60 ceal."
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB051763; BAB18572.1; -.
SEQUENCE 677 AA; 76637 MW; 4B414DCC3F1A3590 CRC64;
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID⇔9606;
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09H3MB;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
NADPH-CYTOCHROME P-450 REDUCTASE.
Pfam; PF00667; FAD_binding; 1. PRINTS; PR00369; FLAVODOXIN. PRINTS; PR00371; FPNCR.
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1 RMTLVFGSRRPDEDHIYQ 18 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 1 NSZA-HUMAN 139 40 39 40 39 40 40 39 41 39 42 39 43 39 44 39 44 39 45 39 46 39 47 39 48 39 48 39 48 39 48 39 49 39 40 01-FEB-1994 DT 01-FEB-1994	wwaadadadada H4	STAND, 92; 0607; (Rel. 28 (Rel. 33 (Rel. 39 SYNTHAS,	(Human) etazom; etazom; theria; 606; M N.A. 7 Forenst Lowenst	loning a epatocyt. Acad. Sc. M N.A. ectal ad 2282; Pul , Laubacl n and cDl tumor co	M N.A. rocytes; 8614; Pul Palmer Hall V.S aracteri; tric oxic	M N.A. ular choi ular choi lbe G., bi ltric oxi and anal phys. Act M N.A. a; a; a; a; a; a; a; b; a; a; b; a; a; a; b; a; a; a; b; a; a; a; a; a; b; a;
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 "Structural characterization of nitric oxide synthase isoforms reveals striking active-site conservation."; Nat. Struct. Biol. 6:233-242(1999).
--- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 74-504.
MEDLLINE=999400067; PubMed~10409685;
Li H., Raman C.S., Glaser C.B., Blasko E., Young T.A., Parkinson J.F.,
Whitlow M., Poulos T.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Crystal structures of zinc-free and -bound heme domain of human inducible nitric-oxide synthase. Implications for dimer stability and comparison with endothelial nitric-oxide synthase.";
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                                                                                                                                                          Guo F.H., de Raeve R.H., Rice T.W., Stuehr D.J., Thunnissen F.B.J.M., Erzurum S.C.;
                                                                                                                                                                                       'Continuous nitric oxide synthesis by inducible nitric oxide synthase
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                                   TISSUE-Glioblastoma;
MEDLINE-95155267; PubMed-7531687;
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Floning and functional expression of human inducible nitric oxide synthase (NOS) cDNA from a glioblastoma cell line A-172.";
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                                                                                                                                                                                                                                                    TISSUE-Cardiac myocytes;

MEDLINE-97304504; PubMed-9160867;

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Hatakayama K., Geller D.A., Mickle D.A.G., Simmons R.L.,
Billiar T.R.;

"Dedifferentiated human ventricular cardiac myocytes express
inducible nitric oxide synthase mRNA but not protein in response t
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BEDLINE-299173237, PubMed-110074942.

Fischmann T.O., Hruza A., Nu X. D., Fossetta J.D., Lunn C.A.,

Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taylor B.S., Alarcon L.H., Billiar T.R.; "Inducible nitric oxide synthase in the liver: regulation and
                                                                                                                                                                                                    in normal human airway epithelium in vivo.";
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Biophys. Res. Commun. 205:85-91(1994).
                                                                                                                                                                                                                                                                                                                                                      Mol. Cell. Cardiol. 29:1153-1165(1997)
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MEDLINE~95165725; PubMed~7532248;
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MEDLINE-98389865; PubMed-9721329;
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TISSUE-Airway epithelium;
MEDLINE-95372368; PubMed-7544004;
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Kidney Int. 46:1043-1049(1994).
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                                                                                                     THE ENZYME (BY SIMILARITY).

-1- ENZYME REGULATION REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST WITH MOUSE NOS2). ASPIRIN INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CATALITY ACTIVITY (BY SIMILARITY).

-1- SUBDIT: HOMODIMER.
-1- TISSUE SPECIFICITY: EXPRESSED IN THE LIVER, RETINA, BONE CELLS AND AIRMAY EPITHELIAL CELLS OF THE LUNG. NOT EXPRESSED IN THE
                                                   NITRIC OXIDE + N NADP(+).
COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.

CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +
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FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
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EMBL; U05810; AAA56666.1; -...
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Pfam: PF00667; FAD_binding; 1.
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NP_BIND
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NADP (ADP PART) (BY SIMILARITY).

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NP_BIND
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SEQUENCE
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Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;
Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;
Three members of the nitric oxide synthase II gene family (NoS2A,
NOS2B, and NOS2C) colocalize to human chromosome 17. ";
Genomics 27:526-530(1995).
C-1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO
MEDIATES TUNGTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO
MEDIATES TUNGTIONE. LANGININE + N NADPH + M O(2) = CITRULLINE +
NITRIC OXIDE + N NADP(+).
C-1- CAPALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +
NITRIC OXIDE + N NADP(+).
C-1- CAPALYTIC BODY (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
THE ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       ;
0
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Bone marrow macrophage;
MEDLINE=95238970; PubMed=7536776;
Adler H., Frech B., Thoeny M., Pfister H., Peterhans E., Jungi T.W.;
Inducible nitric oxide synthase in cattle. Differential cytokine regulation of nitric oxide synthase in bovine and murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                       NOS2_BOVIN STANDARD; PRT; 246 AA. Q27995; Q27985; Q27995; Q27985; Q27995; Q27985; Q27997 (Rel. 35, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) NITRIC OXIDE SYMTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II) (INDUCIBLE NOS) (INOS) (NOSII) (FRAGMENTS).
                                                                       ;
0
                    Score 92; DB 1; Length 1153;
Pred. No. 9.2e-08;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001433; -.
Pfam; PF00175; oxidored_fad; 1.
Oxidoreductase; NADP; FAD; FWN; Calmodulin-binding; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HÖMODIMER (BY SIMILARITY). SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Pulmonary artery;
MEDLINE=96047340; PubMed=7558036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         macrophages.";
J. Immunol. 154:4710-4718(1995)
                                                                       ;
0
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                    94.8%;
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                                                                                                                                                   1009 RMTLVFGCRRPDEDHIYQ 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-110 FROM N.A.
                                                                                                                       1 RMTLVFGSRRPDEDHIYQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U18331; AAC48479.1;
                      Query Match
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multigene family,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
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NOS2_BOVIN

ID NOS2_BOVIN

DT NOS2_BOVIN

DT 30-MAY.

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DT 30-MAY.

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DT 30-MAY.

DE NITRIC

GN Box tai

OC Box tai

NOS2.

RA Adler

RT 1 Induc

CC -1- SI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-NEW ZEALAND WHITE; TISSUE-Heart;
Broner C.W., Eledath F.M.;
"Rabbit iducible nitric oxide synthase gene-NOS II.";
Submitted (JAN-11997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
- WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE + NITRIC OXIDE + N NADP(+).
-!- COFACTOR: HEME. BIRDS ONE MOLE EACH OF FED AND FMN. ALSO REQUIRES TETRAHYDROSIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF THE ENZYME (BY SIMILARITY).
-!- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY
                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC ONTES SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
(INDUCIBLE NOS) (INOS) (FRAGMENT).
                                                                                                                              ö
                                                                           Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
                                                                           Score 81; DB 1; Length 246
Pred. No. 1.3e-06;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW; A0AlD303C57F0EEC CRC64;
28748 MW; 87C2E330C86A27F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00667; FAD_binding; 1. Pfam; PF00175; oxidored_fad; 1
                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
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                                                                           83.5%;
                                                                                                                                                                                                           133 RMTLVFGCRRPEEDHLY 149
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                                                                                                                                                                                 1 RMTLVFGSRRPDEDHIY 17
                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001433; -. InterPro; IPR003097; -.
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246 AA;
                                                                           Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9986;
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274
349
447
496
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019114;
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Biochim. Biophys. Acta 1218:421-424(1994).

vascular smooth muscle cells.";

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-9221515; PubMed-7682072; Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.; "Hepatocytes and macrophages express an identical cytokine inducible nitric oxide synthase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY; TISSUE-Aorta;
MEDILNE-9432531; PubMed=7519446;
Geng Y.J., Almquist M., Hansson G.K.;
"CDNA cloning and expression of inducible nitric oxide synthase from
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-WISSTAR; TISSUE-Pancreatic islets;
MEDLINE-95309542; PubMed-7540573;
MEDLINE-95309542; PubMed-7540573;
Karlsen A.E., Andersen H.U., Vissing H., Larsen P.M., Fey S.J.,
Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,
Mandrup-Poulsen T., Boel E., Nerup J.;
"Cloning and expression of cytokine-inducible nitric oxide synthase
Diabetes 44:753-758(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SPRAGUE-DAWLEY; TISSUE-Astrocytes;
MEDLINE-94213199; bubmed-7513765;
Galea E., Reis D.J., Felnstein D.L.;
"Cloning and expression of inducible nitric oxide synthase from rat
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-Vascular smooth muscle;
TESUE-Vascular smooth muscle;
Muscline-93191721: Pubmed-7680561;
Nunokawa Y., Ishida N., Tanaka S.;
"Cloning of inducible nitric oxide synthase in rat vascular smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Υ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                calmodulin-dependent nitric-oxide synthase from rat liver and its expression in COS 1 cells.";
                                                                                                                                                                                      OG6518; P97774; O35765; O35766; Q64558; Q64005; Q63267; Q1-JUN-1994 (Rel. 29, Created) O1-G7-1996 (Rel. 34, Last sequence update) O1-OCT-1996 (Rel. 34, Last sequence update) NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II) NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II) NOS?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Liver;
MEDLINE-94039959; PubMed-7693462;
Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki Rawasaki H., Sugimura T., Esumi H.;
"Molecular cloning of a cDNA encoding an inducible
                                           ö
83.5%; Score 81; DB 1; Length 496; 77.8%; Pred. No. 2.8e-06; 1ve 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 191:767-774(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 191:89-94(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN SPRAGUE - DAWLEY; TISSUE Hepatocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurosci. Res. 37:406-414(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eur. J. Blochem. 217:37-43(1993).
                                                                                            380 RMTLVFGCRHPEEDHLYQ 397
                                                                           1 RMTLVFGSRRPDEDHIYQ 18
                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       muscle cells.";
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     Query Match
                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michel T., Balligand J.-L.;
Michel T., Balligand J.-L.;
"Isolation and characterization of iNOS from rat cardiocytes.";
"Isolation and characterization of EMBL/Genbank/DDBJ databases.
"In FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.
--- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) ° CITRULLINE + NITRIC OXIDE + N NADPH - N N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 426-788 FROM N.A.
STRAIN DAHL/RAPP SALT SENSITIVE STRAIN; TISSUE-Vascular smooth muscle;
MEDLINE-98195092; Pubmed-9535415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FWN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNITY: HOMODIMER (BY SIMILARITY).
TISSUE SPECIFICITY: IN NORMAL KIDNEY, EXPRESSED PRIMARILY IN THE MEDULLARY THICK ASCENDING LIMB, WITH MINON AMOUNTS IN THE MEDULLARY COLLECTING DUCT AND VASA RECTA BUNDLE.
INDUCTION: BY INTERFERON GAMMA AND LIPOPOLYSACCHARIDE.
SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen P.Y., Gladish R.D., Sanders P.W.;
"Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of inducible nitric oxide synthase in rat kidney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-WISTAR; TISSUE-Renal glomerulus;
Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S.;
"Advances in the studies of NO synthesis regulation in mesanglial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Location of an inducible nitric oxide synthase mRNA in the normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ω.
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                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE~97070590; Pubmed~8913516;
Tsutsumishita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,
                                                                                                 Kosuga K., Yul Y., Hattori R., Sase K., Elzawa H., Aoyama
Janue R., Sasayama S.;
                                                                                                                                                                                    "Cloning of an inducible nitric oxide synthase from rat polymorphonuclear neutrophils."; Endothelium 2:217-221(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY; TISSUE-Renal glomerulus; MEDLINE-94276509; PubMed-7516453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lung, and uterus.";
Biol. Pharm. Bull. 19:1374-1376(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               salt-sensitive rats.";
Hypertension 31:918-924(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                           Futaki S., Niwa M.;
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Myocardium;
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RESULT 5
NS2D_HUMAN

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CALMODULIN'BINDING (POTENTIAL).
FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
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Pred. No. 6.8e-06;
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                                                                                                                                                                                                                     AF006619; AAC16401.1; -. AF006620; AAC16402.1; -.
                                                                                                                                                                                                                                                                       EMBL, U48829; AAB18620.1; -. EMBL; S71597; AAB31028.2; -. EMBL; L36063; AAC02242.1; -.. PIR; JC1472; JC1472.
                                                                                                                      L12562; AAA41720.1; ... X76881; CAA54208.1; -.. D44591; BAA07994.1; -.. D83661; BAA12035.1; -..
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77.8%;
                                                                       AAC13747.1;
BAA02090.1;
                       BAA03138.1;
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InterPro; IPR001094; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001433; -. InterPro; IPR001709; -.
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                                                                       U03699;
D12520;
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NP_BIND
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                                                                                                                                              EMBL;
EMBL;
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EMBL;
EMBL;
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                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                                                       NILLIC OXIGE 2:242-249(1998).

-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS. THRACOPHAGES, NO MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS. MAY BE INVOLVED IN THE PATHOGENESIS OF DILATED CARDIOMYOPATHY OR OF EXERCISE INTOLERANCE OBSERVED IN PATIENTS WITH CHRONIC HEART FAILURE.
-!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE + NITRIC OXIDE + N NADP(+).
-!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEME (BY SIMILARITY).

CALMODULINE BINDING (POTENTIAL).

CALMODULINE PART) (BY SIMILARITY).

FAD (ADP PART) (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

NADP (RIGOSE PART) (BY SIMILARITY).

NADP (RIGOSE PART) (BY SIMILARITY).

ZINC (BY SIMILARITY).

ZINC (BY SIMILARITY).
NS2D_HUMAN STANDARD; PRT; 1147 AA.
060501; 060604;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
NITRIC OXIDE SYNTHASE, INDUCIBLE IID (EC 1.14.13.39) (NOS, TYPE II D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;
Heme; Zinc; Metal-binding; Multigene family.
BINDING 197 HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HOMODIMER (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED IN THE HEART AND SKELETAL MUSCLE
DURING CHRONIC HEART EALLURE, BUT NOT IN HEALTHY INDIVIDUALS.
SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                    "Complete coding sequence of inducible nitric oxide synthase from human heart and skeletal muscle of patients with chronic heart
                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-Skeletal muscle, and Heart muscle;
MEDLINE-99066690; PubMed-9851365;
Addams V., Krabbes S., Jiang H., Yu J., Rahmel A., Gielen S., Schuler G., Hambrecht R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE ENZYME (BY SIMILARITY).
ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (BY SIMILARITY).
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S (IN AAC83554)
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ZINC
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EMBL; AF051164; AAC83554.1; --
HSSP; P29477; INOC.
InterPro; IPR001094; --
InterPro; IPR001433; --
InterPro; IPR001439; --
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Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
                                                                                                              (INDUCIBLE NOS) (INOS).
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Gaps

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Indels

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RMTLVFGSRRPDEDHIYQ 18

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Best_Local Similarity 77.8 Matches 14; Conservative

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Lee T.D., Ding A., Troso T., Nathan C.;
"Cloning and characterization of inducible nitric oxide synthase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92357701; PubMed-1379716;
Lowenstein C.J., Glatt C.S., Bredt D.S., Snyder S.H.;
"Cloned and expressed macrophage nitric oxide synthase contrasts with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BALB/CBYJ, SJL/J, NOD/LTJ, AND B10.S/J; TISSUE~Spleen;
                                                                                                                                                                                                                                                                     Gaps
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MEDLINE-92210618; PubMed-1372907;
MEDLINE-92210618; C.J., Cunningham J.M.;
"Molecular cloning and functional expression of an inducible nitric oxide synthase from a murine macrophage cell line.";
J. Biol. Chem. 267:6370-6374(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 116-496.
MEDLINE-97477482; PubMed-9334294;
Crane B.R., Arvai A.S., Gachhul R., Wu C., Ghosh D.K., Getzoff E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDINE-960087781; MEDINE-960087781; Pubmed-7503239; Kone B.C., Schwoebel J., Turner P., Mohaupt M.G., Cangro C.B.; "Role of NF-kappa B in the regulation of inducible nitric oxide synthase in an MTAL cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   P29477; 070515; 070516; 01-ARR-1993 (Rel. 25, Created)
01-ARR-1993 (Rel. 25, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC OXIDE SYMTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
(INDUCIBLE NOS) (INOS) (MACROPHAGE NOS) (MAC-NOS).
                                                                                                                                                                                                                                                                   ;
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D -> A (IN AAC83554).

G -> E (IN AAC83554).

P -> O (IN AAC83554).

A -> T (IN AAC83554).

H -> N (IN AAC83554).

T. -> N (IN AAC83554).

E -> K (IN AAC83554).

E -> K (IN AAC83554).

F -> V (IN AAC83554).

F -> V (IN AAC83554).
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No. 6.8e-06; ...
2; Indels
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the brain enzyme.";
Proc. Nati. Acad. Sci. U.S.A. 89:6711-6715(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1144 AA
                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                              Score Pred. 1
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77.8%;
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                                                                                                                                                                                                                                                                                                     1 RMTLVFGSRRPDEDHIYQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse macrophages.";
Science 256:225-228(1992).
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   271
399
640
731
937
1009
11024
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Ma R.Z., Teuscher C
                                                                                                                                                                                                                            Query Match
Best Local Similarity
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1024
1076
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P29477; 070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE ENZYME.

-!- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY.
                                                                                                                                                                              MEDLINE-20031637; PubMed-10562538; Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhui R., Crooks C., Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.; "Inducible nitric oxide synthase: role of the N-terminal beta-hairpin hook and prerin-binding segment in dimerization and tetrahydrobiopterin interaction."; EMBO J. 18:6260-6270(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB-Macrophage;
MEDLINE-95372392; PubMed-7544010;
Amin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,
Weissmann G., Abramson S.B.;
"The mode of action of aspirin-like drugs: effect on inducible nitric
                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.
MEDLINE-98182450; Pubmed-9516116;
Crane B.R., Arvai A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structure of nitric oxide synthase oxygenase dimer with pterin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.
MEDLINE-20031638; PubMed-10562539;
Cane B.R., Rosenfeld R.J., Arval A.S., Ghosh D.K., Ghosh S.,
Tainer J.A., Stuehr D.J., Getzoff E.D.;
"N-terminal domain swapping and metal ion binding in nitric oxide
             "The structure of nitric oxide synthase oxygenase domain and inhibitor complexes.";
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-!- TISSUE SPECIFICITY: MACROPHAGES.
-!- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES.
-!- SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                         OF 77-496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M92649; -; NOT_ANNOTATED_CDS.
EMBL; M4373; AAA39834.1; -:
EMBL; M43428; AAAC52356.1; -:
EMBL; AF065919; AAC17915.1; -:
EMBL; AF065920; AAC17915.1; -:
EMBL; AF065921; AAC17915.1; -:
EMBL; AF065922; AAC17917.1; ALT_INIT.
EMBL; AF065923; AAC17918.2; -:
PIR; A43271; A43271.
                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 279:2121-2126(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthase dimerization.";
EMBO J. 18:6271-6281(1999).
                                                          inhibitor complexes.";
Science 278:425-431(1997).
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D.J., Tainer J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFFECT OF ASPIRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tainer J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          substrate
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TISSUE=Leukocyte;
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SEQUENCE
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NS2B_HUMAN
SO THE THE TENT NAME OF THE PROPERTY OF THE PR
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MEDLINE-98343971; PubMed=9677342;
Shirato M., Sakamoto T., Uchida Y., Nomura A., Ishii Y., Iijima H.,
GOLO Y., Hasegawa S.;
"Molecular cloning and characterization of Ca2+-dependent inducible nitric oxide synthase from guinea-pig lung.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
ZINC.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
NOS, OR NO
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(IN STRAIN BALB/CBYJ).
(IN REF. 4).
(IN REF. 2).
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PRINTS; PR00371; FPNCR.
Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.4%; Score 77; DB 1; Le. 72.2%; Pred. No. 3.3e-05; ive 3; Mismatches 2;
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C -> R (IN S
P -> L (IN S
S -> F (IN S
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Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
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29-MAR-00.
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23-MAR-99.
08-DEC-99.
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                                                                                                                               23-MAR-99
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es 13; Conserv
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3NOD;
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1DD7;
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chem. J. 333:795-799(1998). FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.
                                                                                            -:- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE + NITRIC OXIDE + N NADP(+).

-:- COPACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FWN. ALSO REQUIRES TETRAHYDROSIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF THE ENZYME (BY SIMILARITY).

-:- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST
                                                                                                                                                                                                                                                                                                                                           -i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- TISSUE SPECIFICITY: EXPRESSED IN THE LUNG AND COLON. NOT DETECTED IN THE HEART, AORTA, LIVER, KIDNEY, AND SPLEEN.
-i- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS) IN KIDNEY, SPLEEN, AND COLON. EXPRESSION IS REDUCED IN THE PRESENCE OF LPS IN LUNG.
-i- SIMILARITY: BELONGS TO THE NOS FAMILY.
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BINDING 199 199 HEME (BY SIMILARITY).

DOMAIN 508 528 CALMODULIN-BINDING (POTENTIAL).

NP_BIND 622 653 FMN (PYRIMIDINE PART) (BY SIMILARITY).

NP_BIND 766 777 FAD (ADP PART) (BY SIMILARITY).

NP_BIND 902 912 FAD (FLAVIN PART) (BY SIMILARITY).
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
310-MAY-2000 (Rel. 39, Last annotation update)
NITRIC-OXIDE SYNTHASE IIB (EC 1.14.13.39) (NOS, TYPE II B) (NOSIIB)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAD (FLAVIN PÁRT) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
W, 6D295A2486DB50E CRC64:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR003097; -...
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF027180; AAC33177.1; -.
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Best Local Similarity 72.2
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR001094; -. Interpro; IPR001433; -. Interpro; IPR001709; -.
                                                                                                                                                                                                                                                                                                                     WITH MOUSE NOS2).
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SEQUENCE FROM N.A.
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1075
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2 MTLVFGSRRPDEDHIYQ 18
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NP_BIND
METAL
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NP_BIND
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                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                     -:- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.
-:- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) - CITRULLINE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-96216113; PubMed-8662618;

Lin A.W., Chang C.C., McCormick C.C.;

"Molecular cloning and expression of an avian macrophage nitric-oxide synthase cDNA and the analysis of the genomic 5'-flanking region.";

J. Biol. Chem. 271:11911-11919(1996).
                                                                                                                       NITRIC OXIDE + N NADP(+).
-1- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF THE BNZYME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;
         Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G., Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.; Three members of the nitric oxide synthase II gene family (NOS2A, NOS2B, and NOS2C) colocalize to human chromosome 17.; Genomics 27:526-530(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                              NADP (RIBOSE PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOS2_CHICK STANDARD; PRT; 1136 AA.
090703; Q90677; Q90934;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
(INDUCIBLE NOS) (INOS) (MACROPHAGE NOS).
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                                                                                                                                                                          ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66; DB 1; Length 79; Pred. No. 0.00014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83705AE0C36A94E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                  -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE NOS FAMILY.
MEDLINE-96047340; PubMed-7558036;
                                                                                                                                                                                                                                                                                                                                     EMBL; U18332; AAC50232.1; -. EMBL; U18333; AAC50233.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.0%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8667 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 68.0
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    family.
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79
79 AA;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                           in chick embryonic ventricular myocytes.";
Cardiovasc. Res. 38:405-413(1998).
-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. NO MAY SERVE AS BOTH A
PARACRINE AND AUTOCRINE SIGNAL FOR MODULATING OSTEOCLAST BONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- CATALTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE + NITRIC OXIDE + N NADP(+).

-:- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF THE EMZYME (BY SIMILARITY).

-:- SUBGUIT: HOMODIMER (BY SIMILARITY).

-:- SIMILARITY: BELONGS TO THE NOS FAMILY.
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CALMODULIN BINDING (POTENTIAL).

FAN (PYRINIDINE PART) (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).

ZINC (BY SIMILARITY).
                           Sunyer T., Rothe L., Jiang X., Osdoby P., Collin-Osdoby P.; "Proinflammatory agents, IL-8 and IL-10, upregulate inducible nitric oxide synthase expression and nitric oxide production in avian osteoclast-like cells."
                                                                                                                                                                                                                                                                                                                           Shimizu T., Kinugawa K., Sugishita Y., Sugishita K., Harada K.,
Matsui H., Kohmoto O., Serizawa T., Takahashi T.;
"Molecular cloning and expression of inducible nitric oxide synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0.012;
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Pred. No.
                                                                                                                                                                 Cell. Biochem. 60:469-483(1996)
                                                                                                                                                                                                                                                                 TISSUE-Heart;
MEDLINE-98375063; PubMed-9709401;
MEDLINE-96252270; PubMed-8707887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00175; oxidored_fad; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
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                                                                                                                                                                                                                                  SEQUENCE OF 646-986 FROM N.A.
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64.7%;
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STRAIN-168
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NOS3_RAT
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Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;
"Three members of the nitric oxide synthase II gene family (NOS2A,
"Three members of the nitric oxide synthase II gene family (NOS2A,
"Three members of the nitric oxide synthase II gene family (NOS2A,
"Three members of the nitric oxide synthase II gene family (NOS2A,
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"Three members of the nitric oxide synthase II gene family (NOS2A,
"Three members of the nitric oxide for human chromosome 17.",
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Heme; Multigene family.
                                                                                                                                        330-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC-OXIDE SYNTHASE IIC (EC 1.14.13.39) (NOS, TYPE II C) (NOSIIC)
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADP (RIBOSE PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59; DB 1; Length 69;
Pred. No. 0.0019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2C29D595F93FB293 CRC64;
                                                                                                         69 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1054 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBUNIT: HÖMODIMER (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Leukocyte;
MEDLINE=96047340; PubMed=7558036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U18335; AAC50245.1; -.
EMBL; U18334; AAC50245.1; JOINED.
HSSP; P00388; 1AMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8432 MW;
1007 MILLFGCRHPDMDHIYK 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RMTLVFGSRRPDEDHIYQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 60.8
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 AA;
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYPE_BACSU
ID CYPE_BACSU
AC 008336;
                                                                                                                                                                                                                     (FRAGMENT).
                                                                                                           NS2C_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
                                                                                                                            014961
                                                                       RESULT 10
NS2C_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FERROCYTOCHROME.
-!- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FMN (BY SIMILARITY).
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTIÓN: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P450 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PROBMBLE BIFUNCTIONAL P-450 NADDH-P450 REDUCTASE 2 [INCLUDES:
CYTOCHROME P450 102 (EC 1.14.14.1); NADPH-CYTOCHROME P450 REDUCTASE
                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97453479; pubMed=9308178; Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J., Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J., Duesterhoeft A., Ehrlich S.D.; "Sequence of the Bacillus subtilis genome region in the vicinity of the lav operon reveals two new extracytoplasmic function RNA polymerase sigma factors SigV and SigZ."; Microbiology 143:2939-2943(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEME (BY SIMILARITY).

W; 705F8E27866CA110 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NADPH-P-450 REDUCTASE
                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118675 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | || || || || || || || 937 LYFGCRRPDHDDLYR 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LVFGSRRPDEDHIYQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1054 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                      CYPE OR CYPÍOZA3.
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P450 FAMILY.
                                                                                                                                                                                                                                                             NCBI_TaxID=1423;
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NOS3_RAT STANDARD; PRT; 919 AA.
062600; 088672; 089041; 062734;
01-NOV-1997 (Rel. 35, Created)
30-NAY-2000 (Rel. 39, Last sequence update)
30-NAX-2000 (Rel. 39, Last annotation update)
NITRIC-OXIDE SYNTHASE, ENDOTHELIAL (EC 1.14.13.39) (EC-NOS) (NOS, TYPE (FRAGMENTS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: EXPRESSED CONSTITUTIVELY BY VASCULAR RENOTHELIUM. DETECTED IN ALVEOLAR AND SEROSAL EPITHELIAL CELLS AS WELL AS IN ENDOTHELIAL CELLS IN ONE DAY OLD RAT. IN ADULT LUNG, DETECTED IN RARE ENDOTHELIAL CELLS.

BEYELOPHENTAL STAGE: DETECTED AT HIGH LEVELS IN LUNG DURING THE LATE FETAL AND POSTNATAL PERIOD AT LOWER LEVELS IN ADULT. SIMILARLY: BELONGS TO THE NOS FAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Downregulation of endothelial nitric oxide synthase (NOS III) in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY, TISSUE-Lung; MEDLINE-SPRAGUE-DAWLEY, TISSUE-Lung; MEDLINE-95250990; PubMed-7537461; Kawai N., Bloch D.B., Filippov G., Rabkina D., Suen H.C., Losty P.D., Janssens S.P., Zapol W.M., de la Monte S., Bloch K.D.; "Constitutive endothelial nitric oxide synthase gene expression is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS.
CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +
NITRIC OXIDE + N NADP(+).
COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulated during lung development.";
Am. J. Physiol. 268.L589-L595(1995).
-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A CGMP-MEDIATED SIGNAL TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-INDUCED ANGIGGENESIS IN CORNORAR VESSELS AND
                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minchenko A.G., Armstead V.E., Opentanova I.L., Lefer A.M.; "Endchhelin-1, endcthelin receptors and ecNOS mRNA expression in vital organs during traumatic shock in rats."; submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toporsian M., Govindaraju K., Nagi M., Eidelman D., Thibault G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kone B.C.; "Differential expression and induction of mRNAs encoding two inducible nitric oxide synthases in rat kidney."; Kidney Int. 46:653-665(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mohaupt M.G., Elzie J.L., Ahn K.Y., Clapp W.L., Wilcox C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Cloning and expression of the rat endothelial nitric oxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aorta following in-vivo hypoxia.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 288-487 AND 678-919 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 742-859 FROM N.A. STRAIN-SPRAGUE-DAWLEY; TISSUE-Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY;
MEDLINE-95089280; Pubmed-7527874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seidel B., Jiang L., Wolf G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 448-677 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 745-807 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-287 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ward M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthase.
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Ruettinger R.T., Wen L.-P., Fulco A.J.;
"Coding nucleotide, 5' regulatory, and deduced amino acid sequences of P-450BM-3, a single peptide cytochrome P-450:NADPH-P-450 reductase from Bacillus megaterium.";
J. Biol. Chem. 264:10987-10995(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase, NADP; FAD; FMN; Calmodulin-binding; Myristate;
Lipoprotein; Palmitate; Calcium-binding; Heme; Zinc; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
MYRISTARE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
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01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
BIEUNCTIONAL P-450:MADPH-P450 REDUCTASE (CYTOCHROME P450(BM-3))
(P450BM-3) [INCLUDES: CYTOCHROME P450 102 (EC 1.14.14.1); NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4)].
CYTOCHROME P450 REDUCTASE (EC 1.6.2.4)].
Bacillus megaterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALMODULIN-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 919,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW; BF2EAC391C86650F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51; DB 1;
Pred. No. 0.69;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1048 AA.
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NCBI_TaxID=1404;
                                                                                                                                                                                                                                                                                 U02534; AAA96141.1; -. AJ011116; CAA09494.1; -. AF093837; AAC64178.1; -.
                                                                                                                                                                                                                                  EMBL; AF085195; AAC34677.1; -. EMBL; AJ011115; CAA09493.1; -.
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PRINTS; PR00371; FPNCR.
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Pfam; PF00667; FAD_binding;
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P29477; INOC.
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Best Local Similarity
Thes 10; Conserve
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SEQUENCE FROM N.A.
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932 LYFGCRSPHEDYLYQ 946
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Matches 9; Conserv
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PR PDB; 2HPD; 31-0CT-93.

PDB; 2HPD; 31-0CT-93.

PDB; 1FAG; 12-FEB-97.

PDB; 1FAG; 12-FEB-97.

PDB; 1FAG; 12-FEB-97.

R DDB; 1FAH; 12-FEB-97.

R InterPro; IPR001128; -...

R InterPro; IPR001433; -...

R InterPro; IPR003403; -...

R InterPro; IPR003404; -...

R Pfam; PF00175; Oxidored_fad; 1...

R Pfam; PR00175; Oxidored_fad; 1...

R PRINTS; PR00464; EP4501.

R PROSITE; PS00086; CYTCCHROME P450; 1.

R Waltifunctional enzyme; FMN; FAD; Flavoprotein; 3D-structure; NADP.

INT_MET
                                                                                                                                                                                                                                                                                                   complex.";

broc. Natl. Acad. Sci. U.S.A. 96:1863-1868(1999).

1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOXYGENASE CATALYSES

HYDROXYLATION OF MEDIUM AND LONG-CHAIN FATTY ACIDS AT OMEGA-1,

OMEGA-2 AND OMEGA-3 POSITIONS, WITH OPPIMMY CHAIL LENGTHS OF 14-16

CARBONS (LAURIC, MYRASTIC, AND PALMITIC ACIDS). THE REDUCTASE

DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
                                                                                                                                     "Crystal structure of hemoprotein domain of P450BM-3, a prototype for microsomal P450's."; Science 261:731-736(1993).
                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1-471.
MEDLINE=97185914; PubMed=9033595;
Li H Y., Poulos T.L.;
"The structure of the cytochrome p450BM-3 haem domain complexed with the fatty acid substrate, palmitcheic acid.";
Nat. Struct. Biol. 4:140-146(1997).
                                                                                                                                                                                                                                                                                                                                                                                                 2 FERROCYTOCHROME.
-1- COFACTOR: BINDS ONE MOLE BACH OF FAD AND FWN.
-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                  "Fatty acid monooxygenation by P450BM-3: product identification and proposed mechanisms for the sequential hydroxylation reactions."; Arch. Blochem. Blophys. 292:20-28(1992).
                                                                                             X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-471.
MEDLINE-93342510; PubMed-8342039;
Rayichandran K.G., Boddupalli S.S., Hasemann C.A., Peterson J.A.,
                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.03 ANGSTROMS).
MEDLINE-99162523; PubMed-10051560;
Sevrioukova I.F., Li H., Zhang H., Peterson J.A., Poulos T.L.;
"Structure of a cytochrome P450-redox partner electron-transfer
                     MEDLINE-92088245; PubMed-1727637;
Boddupalli S.S., Pramanik B.C., Slaughter C.A., Estabrook R.W.,
                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME = NADP(+) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J04832; AAA87602.1; -.
[2]
CHARACTERIZATION.
                                                                                                                             Deisenhofer J.;
                                           Peterson J.A.;
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us-08-833-506c-31.rsp

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Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;
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BINDING
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             RESULT 14

NOS3_MOUSE
D NOS3_MOUSE
STANDARD; PRT; 1201 AA.

AC P70313; 055056;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DF 30-MAY-2000 (Rel. 30, Last sequence u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gregg A.R., Schauer A., Shi O., Liu Z., Lee C.L., O'Brien W.E.; "Limb reduction defects in endothelial nitric oxide synthase deficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION.

MEDILIPRE-99061722; PubMed-9843834;
Gregg A.R., Schauer A., Shi O., Liu Z., Lee C.G.L., O'Brien W.E.;

"Limb reduction defects in endothelial nitric oxide synthase-deficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Am. J. Physiol. 275:H2319-H2324(1998).

-I. Physiol. 275:H2319-H2324(1998).

-I. Physiol. 275:H2319-H2324(1998).

-I. Physiol. 275:H2319-H2324(1998).

-I. PROUTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN VASCULAR SMOOTH MUSCLE BELAXATION THROUGH A CGMP-MEDIATED SIGNAL TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH FANNSDUCTION PATHWAY. NO MEDIATES IN CORONARY VESSELS. AND PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS. MAY PLAY A SIGNIFICANT ROLE IN NORMAL AND ABNORMAL LIMB DEVELOPMENT.

-I. CATALYTIC CATIVITY: L-ARGININE + N NADPH + M O(2) - CITRULLINE + NITRIC OXIDE + N NADP(+).

-I. COFACTOR: HEME. BINDS (+).
                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Fetal heart;
MEDLINE-96350460; PubMed-8764825;
Gnanapandithen K., Chen Z., Kau C.-L., Gorczynski R.M., Marsden P.A.;
"Cloning and characterization of murine endothelial constitutive nitric oxide synthase.";
                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID>10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mice.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
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-!- SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blochim. Blophys. Acta 1308:103-106(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-53 FROM N.A. TISSUE-FEtal heart;
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MGD; MGI:97362; NOS3.
InterPro; IPR001094; -.
InterPro; IPR001433; -.
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NOS3_HUMAN STANDARD; PRT; 1202 AA.
P29474, Q14521; 014444, Q13662;
01-APR-1993 (Rel. 25, Created)
01-JUL-1993 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRC-OXIDE SYNTHASE, ENDOTHEIAL (EC 1.14.13.39) (EC-NOS) (NOS, TYPE)
111) (NOSIII) (ENDOTHEIAL NOS) (ENOS) (CONSTITUTIVE NOS) (CNOS).
                                                       BY SIMILARITY.

HEME (BY SIMILARITY).

CALMODULIN-BINDING (POTENTIAL).

FAN (PYRIMIDINE PART) (BY SIMILARITY).

FAD (ADP PART) (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

NADP (RIBOSE PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).

PALMITATE (BY SIMILARITY).

PALMITATE (BY SIMILARITY).

PALMITATE (BY SIMILARITY).

ZINC (BY SIMILARITY).

ZINC (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.P., Shimouchi A., Quertermous T., Bloch D.B., Bloch K.D.;
Chem. 267:22694-22694(1992).
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Lipoprotein; Palmitate; Calcium-binding; Heme; Zinc; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marsden P.A., Heng H.H., Scherer S.W., Stewart R.J., Hall A.V., Shi X.M., Tsui L.C., Schappert K.T.; Sztructure and chromosomal localization of the human constitutive endothelial nitric oxide synthase gene."; J. Biol. Chem. 268:17478-17488(1993).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.92;
2; Mismatches 5; Indels
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DA37ABAC947DABD5 CRC64;
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MEDLINE⇔92354731; PubMed∴1379542;
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58.8%;
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Best Local Similarity 58.8
Matches 10; Conservative
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                              Multigene family.
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647
791
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1008
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and for commercial

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us-08-833-506c-31.rsp

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(See http://www.isb-sib.ch/announce/
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CALMODULIN-BINDING (POTENTIAL).
FAMOOULINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (RIBOSE PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
MYRISTATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
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Pfam; PF00175; oxidored_fad; 1.
PRINTS; PR00375; ELAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;
Lipoprotein; Palmitate; Disease mutation; Calcium-binding; Heme;
Zinc; Metal-binding; Multigene family; 3D-structure.
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/FTId=VAR_008037.
S -> R (IN REF. 8).
G -> S (IN REF. 9).
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EMBL; X76315; CAA53950.1; JOINED.
EMBL; X76316; CAA53950.1; JOINED.
EMBL; D26607; BAA05652.1; -
EMBL; L23210; AAA36373.1; -
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InterPro; IPR001433; -.
InterPro; IPR001709; -.
InterPro; IPR003097; -.
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PIR; A42867; A42867.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A missense Glu298Asp variant in the endothelial nitric oxide synthase gene is associated with coronary spasm in the Japanese.";
Hum. Genet. 103:65-69(1998).

-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A CGMP-MEDIATED SIGNAL TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-INDUCED ANGIOGENEETS IN CORONARY VESSELS AND PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS.

-!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE + NITRIC OXIDE + N NADP(+).

-!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sase K., Michel T.;
"Expression of constitutive endothelial nitric oxide synthase in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98407797; PubMed-9737779;
Yoshimura M., Yasue H., Nakayama M., Shimasaki Y., Sumida H.,
Sugiyama S., Kugiyama K., Ogawa H., Ogawa Y., Saito Y., Miyamoto Y.,
                                                                                                 Nadaud S.A., Bonnardeaux A., Lathrop M., Soubrier F.; "Gene structure, polymorphism and mapping of the human endothelial nitric oxide synthase gene.";
                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-9433373; PubMed=7519987;

Miyahara K., Kawancor T., Sase K., Yui Y., Toda K., Yang L.X.,

Hattori R., Aoyama T., Yamamoto Y., Doi Y., Ogoshi S.,

Hashimoto K., Kawai C., Sasayama S., Shizuta Y.;

Cloning and structural characterization of the human endothelial

nitric-oxide-synthase gene.;

Eur. J. Blochem. 223:719-726(1994).
                                                                                                                                                                                                                                                                                                                                                                                Robinson L.J., Weremowicz S., Morton C.C., Michel T.; "Isolation and chromosomal localization of the human endothelial nitric oxide synthase (MoS3) gene."; Genomics 19:350-357(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99173237; PubMed-10074942;
Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,
Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.
Weber P.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural characterization of nitric oxide synthase isoforms reveals striking active-site conservation."; Nat. Struct. Biol. 6:233-242(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- TISSUE SPECIFICITY: PLATELETS.
-1- DISEASE: DEFECTS IN NOS3 ARE INVOLVED IN CORONARY SPASM.
-1- SIMILARITY: BELONGS TO THE NOS FAMILY.
   Liao J.K.;
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN.
                                                                                                                                                 Biochem. Biophys. Res. Commun. 198:1027-1033(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [10]
X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                  TISSUE=Placenta;
MEDLINE=94245207; PubMed=7514568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Platelet;
MEDLINE=96077182; PubMed=7475956;
                                                                                MEDLINE=94161710; PubMed=7509596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT CORONARY SPASM ASP-297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               blood platelets.";
Life Sci. 57:2049-2055(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 410-527 FROM N.A.
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566 566 V -> W (IN REF. 6).
1149 1149 R -> RQ (IN REF. 7).
1193 1193 D -> E (IN REF. 6).
1202 AA; 133157 WW; 93D127D6C14AC92E CRC64;
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; 0 Gaps .; 0 Query Match 52.6%; Score 51; DB 1; Length 1202; Best Local Similarity 58.8%; Pred. No. 0.92; Matches 10; Conservative 2; Mismatches 5; Indels

Search completed: September 10, 2001, 14:09:54 Job time: 563 sec

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version 4.5
- 2000 Compugen Ltd.
    GenCore
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OM protein - protein search, using sw model

September 10, 2001, 14:01:15 Run on:

' Search time 42.28 Seconds
(without alignments)
32.430 Million cell updates/sec

1 RMTLVFGSRRPDEDHIYQ 18 US-08-833-506C-31 97 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	& Query Match	94.8	83.5	83.5	83.5	83.5	83.5	83.5	83.5	79.4	71.1	71.1	0.89	8.09	53.6	52.6	52.6	52.6	52.6	52.6	52.6	52.6	52.6	50.5	50.5	50.5	50.5	49.5	47.4	46.4
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## ALIGNMENTS

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nitric-oxide synthase (EC 1.14.13.39), inducible - human

C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 16 Feb-1996 #text_change 20-Jun-2000
C; Date: 16 Feb-1996 #sequence_revision 16 Feb-1996 #text_change 20-Jun-2000
C; Accession: A49676; JX0345; G01947; I3893; S47566; A47475
R; Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; Hall, V.S.; Proc. Natl. Acad. Sci. U.S.A. 90, 11419-11423, 1993
A; Title: Cloning, characterization, and expression of a cDNA encoding an inducible ni A; Reference number: A49676; MUID:94068614

A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Reduca: 1-1153 (RSA)
A; Cross-references: EMBL: X73029; NID:9441452; PIDN:CAA51512.1; PID:9441453
B; Hokari, A.; Zeniya, M.; Esumi, H.
J. Biochem. 116, 575-581, 1994
A; Title: Cloning and functional expression of human inducible nitric oxide synthase (A; Reference number: JX0345; MUID:95155267
A; Accession: JX0345

A; Residues: 1-607, 'L', 609-1153 <HOK>
A; Cross-references: DDBJCD26525; NID:95326; PIDN:BAA05531.1; PID:91228940
A; Experimental source: 9140blastoma cell line A-172
R; Park, C.; Park, R.; Krishna, G.
R; Park, C.; Park, R.; Krishna, G.
A; Reference number: G08912
A; Reference number: G08912
A; Accession: G1947
A; Status: translatated from GB/EMBL/DDBJ
A; Accession: G1947
A; Residues: 1-607, 'L', 609-1153 <PAR>
A; Residues: 1-607, 'L', 609-1153 <PARP
A; Residues: 1-607, 'L', 609-1

A.Molecule type: mRNA A.Rolecule type: mRNA A.Residues: 1-675, 'I', 677-932,'G', 934-965,'A', 967-1153 <RE2> A.Residues: 1-675, 'I', 677-932,'G', 934-965,'A', 967-1153 <RE2> A.Cross-references: EMBL: U20141; NID: 9687680; PIDN: AAB60366.1; PID: 9687681 R; Maier, R.; Bilbe, G.; Rediske, J.; Lotz, M. Biochim. Biophys. Acta 1208, 145-150, 1994 A; Title: Inducible nitric oxide synthase from human articular chondrocytes: cDNA clon A; Reference number: S47566; MuID: 94368816

A; Status: preliminary; nucleic acid sequence not shown

A; Molecule type: mRNA A; Residues: 1-22,'G', 24-153,'L',155-176,'V',178-799,'A',801-912,'P',914-1153 <MAI> A; Cross-references: EMBL:U05810; NID:9452487; PIDN:AAA56666.1; PID:9452488 F; Geller, D.A.; Lowenstein, C.J.; Shapiro, R.A.; Nussler, A.K.; Di Silvio, M.; Wang, Proc. Natl. Acad. Sci. U.S.A. 90, 3491-3495, 1993

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Riceng, 1:; Ainquist. A. 1914.424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-424, 411-
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Best Local Similarity
Matches 14; Conserv
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A; Residues: 1-422,'I',424-804,'D',806-830,'SP',833-932,'G',934-965,'A',967-986,'V',988-1
A; Cross-references: GB1109210; NRD:9292241; PIDN:AAA39171.1; PID:9292242
A; Experimental source: hepatocytes
A; Note: sequence extracted from NCBI backbone (NCBIP:129733)
C; Genetics:
A; Gene: GDB:NOS2A; NOS2; INOS
A; Cross-references: GBB:139215; OMIM:163730
A; Map position: 17cen-17q11.2
C; Function:
A; Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C; Function:
A; Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C; Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduce
C; Keywords: calmodulin binding *status predicted
F; 509-529/Region: Calmodulin binding *status predicted
F; 509-529/Region: FAD-Pyrophosphate binding *status predicted
F; 503-5178/Region: FAD-Pyrophosphate binding *status predicted
F; 903-913/Region: RADP-adenine binding *status predicted
F; 1076-1091/Region: NADP-adenine binding *status predicted
F; 200/Binding site: heme iron (Gys) (axial ligand) *status predicted
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C;Species: Bos primiquenius taurus (cattle)
C;Species: Bos primiquenius taurus (cattle)
C;Species: Bos primiquenius taurus (cattle)
C;Saccession: Id-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 11-Jun-1999
C;Saccession: Id-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 11-Jun-1999
C;Saccession: Id-Aug-1996 #sequence_revision Id-Aug-1996 #text_change 11-Jun-1999
C;Satcle: Three members of the nitric oxide synthase II gene family (NOS2A, NOS2B, and NC A;Reference number: A57622; MUID:96047340
A;Reference number: A57622; MUID:96047340
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Residues: 1-136 <a href="https://documence-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-number-review-num
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A;Title: Molecular cloning and expression of inducible nitric oxide synthase from human A;Reference number: A47475; MUID:93234523 A;Accession: A47475
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nitric-oxide synthase (EC 1.14.13.39) - rat
c;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Jun-2000
C;Accession: S47647; JC1472
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                                                                                                                                                       translation
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                                                                                                                                                       Status: preliminary; not compared with conceptual
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Best Local Similarity 94.4
Matches 17; Conservative
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nes 14; Conserv
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C; Species: Rattus norvegicus (Norway rat)
C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C; Accession: 156575
R; Galea, E.; Reis, D.J.; Feinstein, D.L.
J Neurosci. Res. 37, 406-444, 1994
A; Title: Cloning and expression of inducible nitric oxide synthase from rat astrocyte
A; Reference number: 156575; MUID:94231594
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A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1147 <RES>
A; Cross-references: BMBL: U03699; NID:9430718; PIDN:AAC13747.1; PID:9430719
A; Cross-references: BMBL: U03699; NID:9430719
C; Superfamily: nitric-coxide synthase; flavodoxin homology; NADPH--ferrihomoprotein ref; SG-1124/Domain: MDPH--ferrihomoprotein; FAD; flavoprotein; FMN; heme; Iron; me F; S38-674/Domain: flavodoxin homology <FENS
F; S38-674/Domain: flavodoxin homology <FENS
F; S197/Binding site: heme iron (Cys) (axial ligand) #status predicted
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C;Specias: Rattus norvegicus (Norway rat)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Jun-2000
C;Accession: S38253; JN0457
E;Adachl, H.: Ilda, S.: Oguchl, S.; Ohshima, H.: Suzuki, H.: Nagasaki, K.: Kawasaki,
Rint. J. Blochem. 217, 374.3, 1993
A;Title: Molecular cloning of a cDNA encoding an inducible calmodulin-dependent nitri
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Indels
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 04-Mar-2000
C;Accession: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 04-Mar-2000
C;Accession: JC5029
R;Tsutsumishita, Y:; Kawai, Y:; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa Biol. Pharm. Bull. 19, 1374-1376, 1996
A;Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, an A;Reference number: JC5027; MUID:97070590
A;Accession: JC5029
A;Accession: JC5029
A;Accession: JC5029
A;Accession: JC5029
A;Reference number: As sequence not shown
A;Residues: 1-1147 <TSU>
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C. Comment: This protein synthesizes nitric oxide from L-arginine.
C. Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein re C. Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me F. 536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>
F. 538-674/Domain: flavodoxin homology <FLX>
F. 197/Binding site: heme iron (Cys) (axial ligand) #status predicted
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Eur. J. Biochem. 237, 668-673, 1996
A; Title: Molecular cloning of endothelial, inducible nitric oxide synthase gene from A; Reference number: S65440; MUID:96235231
A; Accession: S6540
A; Status: not compared with conceptual translation
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A Residues: 1-117 - SIMA
A Residues: 1-117 - SIMA
C Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein: C Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein: FND; flavoprotein; FMN; heme; iron; if F; 506-535, Fregion: calmodulin binding
F; 536-1124, FOOM and in: NADPH--ferrihemoprotein reductase homology <FEH>
F; 536-1124, FOOM and in: flavodoxin homology <FEX>
F; 539-618, FRegion: binding
F; 599-618, FRegion: binding
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C;Species: Rattus norvegicus (Norway rat)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
C;Accession: S65440
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F:1074-1087/Region: NADPH binding #status predicted
F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted
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Pred. No. 1.1e-05;
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Pred. No. 1.1e-05;
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77.8%;
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Best Local Similarity 77.8
Matches 14; Conservative
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A. Residues: 1-41, 'SS', 44-103,105-190, 'Q', 192-213,'R', 215-247,'T', 249-263,'I', 265-373,'IE
A. Residues: 1-41, 'SS', 44-103,105-190, 'Q', 192-213,'R', 215-247,'T', 249-263,'I', 265-373,'IE
A. Residues: 1-41, 'SS', 44-103,105-180,'Q', 192-213,'R', 215-247,'T', 249-263,'I', 265-373,'IE
A. Residues: 1-41, 'SS', 44-103,105-180, 'RO.
A. Experimental source: 11ver
A. Expe
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A;Title: Cloning and expression of cytokine-inducible nitric oxide synthase cDNA from ra A;Reference number: 153165; MUID:95309542
A;Accession: 153165
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-1147 <RES>
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C;Genetics:
A;Gene. NOS:
C;Genetics:
C;
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                                                                                                    A; Wolecule type: mRNA
A; Residues: 1-1147 - ADA>
A; Cross-references: GB-D12520; NID:g391858; PIDN:BAA02090.1; PID:g391859
A; Experimental source: liver
R; Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.
Biochem. Biophys. Res. Commun. 191, 767-774, 1993
A; Title: Hepatocytes and macrophages express an identical cytokine inducible nitric A; Reference number: JN0457; MUID:93221515
A; Accession: JN0457
A; Status: nucleic acid sequence not shown
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C;Date: 05-May_2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
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nitric-oxide synthase (EC 1.14.13.39) U - rat
     A; Reference number: S38253; MUID:94039059
A; Accession: S38253
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Matches 14; Conserv
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A;Residues: 1-1147 <TSU>
A;Experimental source: lung
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Best Local Similarity
Matches 13; Conserv
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A; Residues: 1-1144 (LTC)
A; Residues: 1-1144 (LTC)
A; Cross-recences: GB:M84373; NID:g200095; PIDN:AAA39834.1; PID:g200096
A; Cross-recences: GB:M84373; NID:g200095; PIDN:AAA39834.1; PID:g200096
B; Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.
Biochem. Biophys. Res. Commun. 191, 767-774, 1993
A; Title: Hepatocytes and macrophages express an identical cytokine inducible nitric oxid
A; Reference number: JN0458
A; Recession: JN0458
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-278, F', 280-682, 'H', 684-937, 939-1144 <WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A. Status: preliminary: not compared with conceptual translation
A. Status: preliminary: not compared with conceptual translation
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Moles sequences: 1-190, 'v', 192-765, 'p', 767-843, 'G', 845-1144 < LOW>
A. Experimental source: BALB/c, RAW 264.7 cells, macrophage
A. Mote: sequence extracted from NCBI backbone (NCBIP:113541)
C. Genetics:
A. Mote: sequence extracted from NCBI backbone (NCBIP:113541)
C. Genetics:
A. Mote: sequence extracted from NCBI backbone (NCBIP:113541)
C. Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reducts (Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reducts (S. Keywords: calmodulin binding; chromoprotein; RAD; flavoprotein; FNN; heme; iron; metal F: 533-1121/Domain: NADPH-ferrihemoprotein reductase homology < FEH>
F: 533-1121/Domain: lavodoxin homology < FEH>
F: 535-671/Domain: lavodoxin homology < FEH>
F: 194/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                A; Residues: 1-1144 AXES-A; Coss-references: GB:M87039; NID:g198406; PIDN:AAA39315.1; PID:g198407
R; Cross-references: GB:M87039; NID:g198406; PIDN:AAA39315.1; PID:g198407
R; Lyons, C.R.; Orloff, G.J.; Cunningham, J.M.
J. Biol. Chem. 267, 6370-6374, 1992
A; Title: Molecular cloning and functional expression of an inducible nitric oxide synths
A; Reference number: A42166; MUID:92210618
A;Title: Cloning and characterization of inducible nitric oxide synthase from mouse macr
A;Reference number: A43271; MUID:92229444
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A Experimental source: liver
R: Experimental source: liver
R: Lowenstein, C.J.: Glatt, C.S.; Bredt, D.S.; Snyder, S.H.
Proc. Natl. Acad. Scl. U.S.A. 89, 6711-6715, 1992
A) Title: Cloned and expressed macrophage nitric oxide synthase contrasts with the brain A; Reference number: A46186; MUID: 92357701
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 21-3a-1997 #sequence_revision 21-Jan-1997 #text_change 20-Jun-2000
C;Accession: JC5027
R;Tsutsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa, Biol. Pharm. Buil. 19, 1374-1376, 1996
A;Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and A;Reference number: JC5027; MUID:97070590
A;Reference number: JC5027
A;Reference number: JC50
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Best Local Similarity 72.2
Matches 13; Conservative
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                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                 Accession: A43271
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 04-Mar-2000
C;Dates: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 04-Mar-2000
C;Accession: JG5028
R;TsutsumMshita, Y:; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa Biol. Pharm. Bull. 19, 1374-1376, 1996
A;Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, an A;Reference number: JC5027; MUID:97070590
A;Reference number: JC5028
A;Status: nucleic acid sequence not shown
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C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein C;Keywords: calmodulin binding stromoprotein; FAD; flavoprotein; FMN; heme; iron; F;191-199/Domain: heme-binding #status predicted <HMB>
F;536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>
F;536-1124/Domain: FMN binding #status predicted <FMN>
F;620-647/Domain: FMN binding #status predicted <FMN>
F;94-775,899-910/Domain: FMD binding #status predicted <FMD>
F;975-993,1054-1067/Domain: NADP binding #status predicted <NDP>
F;975-993,1054-1067/Domain: NADP binding #status predicted <NDP>
F;197/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A;Map postLion: 17913.1-17925
C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein
C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron;
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C; Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 11-Jun-1999
C; Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 11-Jun-1999
C; Accession: 138067
A; Pibloch, K.D.; Wolfram, J.R.; Brown, D.M.; Roberts, J.D.
Genomics 27, 526-530, 1995
A; Title: Three members of the nitric oxide synthase II gene family (NOS2A, NOS2B, A; Reference number: A57622; MUID:96047340
A; Reference number: A57622; MUID:96047340
A; Accession: 138067
A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 69; DB 2;
Pred. No. 0.0013;
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A; Experimental source: strain 168
C; Genetics:
A; Gene: yrhJ
C; Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin C; Superfamily: PADPH--ferrihemoprotein; heme; iron; metalloprotein; monooxygenase; o E; 486-1050/Domain: NDPH--ferrihemoprotein reductase homology cFEH>
E; 488-625/Domain: flavodoxin homology cFELN
F; 403/Binding site: heme iron (Cys) (axial ligand) #status predicted

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Gaps

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4; Indels

Score 52; DB 1; Pred. No. 1; 2; Mismatches

53.6%; 60.0%;

Query Match 53.6 Best Local Similarity 60.0 Matches 9; Conservative

4 LVFGSRRPDEDHIYQ 18

ΟŻ Q

Length 1054;

us-08-833-506c-31.rpr

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nitric-oxide synthase (EC 1.14.13.39) 2C - human (fragment)
N.Alternate names: nitric oxide synthase II
C.Species: Homo sapiens (man)
C.Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 11-Jun-1999
C.Accession: 139204
R.Bloch, K.D.: Wolfram, J.R.: Brown, D.M.: Roberts, J.D.
Genomics 27, 526-530, 1995
A; Fitle: Three members of the nitric oxide synthase II gene family (NOS2A, NOS2B, and NC A; Reference number: A57622; MUID:96047340
A; Reference number: A57622; MUID:96047340
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-69 <a href="https://docsa.references: EMBL:U1835">docsa.references: EMBL:U1835</a>; NID:91050946; PIDN:AAC50245.1; PID:91050948
A; Gene: GDB:NOS2C
A; Cross-references: GDB:547943; OMIM:600720
A; Map position: 17p13.1-17q25
A; Introos.: 33,1
C; Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH.-ferrihemoprotein reduc C; Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; NADP;
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C; Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
C; Accession: A65975
C; Bron, S; Brouillet, S; Bruschi, C.V; Caldwell, B; Capuano, V.; Carter, N.M.; Chan, Eritaich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Haracod, C.R.; Henaut, A.; Hibbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Lu, H.; Masuda, S.; Maueelly, M.; Ogewa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Voshida, K.; Watuhors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Altibors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Altibors: Money and Aprilis.
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N:Contains: NADPH--ferrihemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (EC
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                                                                           Gaps
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   Length 49;
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                                                                           4; Indels
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Score 66; DB 2; I
Pred. No. 0.00013;
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Pred. No. 0.003;
                                                                           1; Mismatches
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68.0%;
72.2%;
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66.7%;
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38 RRTLVFWCRRPDEDRHYR 55
Query Match 68.0°
Best Local Similarity 72.2°
Matches 13; Conservative
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                          G.; Rabkina, D.; Suen, H.C.; Losty, P.D.; Janssen
                                                                                C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change ll-Jun-1999
C; Accession: I51917
R; Kawai, N.; Bloch, D.B.; Filippov, G.; Rabkina, D.; Suen, H.C.; Losty, P.D.; Janssen Am. J. Physiol. 268, L589-L595, 1995
A; Title: Constitutive endothelial nitric oxide synthase gene expression is regulated A; Reference number: I51917; MUID:95250990
A; Accession: I51917
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; 1ron;
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                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-63 <RES>
A;Cross-references: EMBL:U18336; NID:g806761; PIDN:AAC52188.1; PID:g806762
C;Genetics:
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    rat (fragment)

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Pred. No. 0.067;
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Job time: 214 sec
                                                        nitric-oxide synthase (EC 1.14.13.39) 3
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58.8%;
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Best Local Similarity 58.8
Matches 10; Conservative
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RESULT
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Title:

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; Search time 67.08 Seconds (without alignments)
16.268 Million cell updates/sec
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GenCore version 4.5
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human iNOS peptide	Human inOS peptide Human iNOS peptide	Human iNOS (1009-1	Inducible nitric o	Sequence encoded b	Nitric-oxide-synth	Hepatocyte inducib	Human inducible ni	Amino acid sequenc	Human inducible ni
SUMMARIES	AAW81252	AAW812/9 AAW81210	AAW81192	AAW96322	AAR55764	AAR63206	AAR88464	AAW36113	AAB31724	AAB66724
D8	19	19	19	20	15	15	17	19	22	22
% Query Match Length DB ID	81.	18	18	1146	1153	1153	1153	1153	1153	1153
% Query Match	100.0	100.0	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8
Score	97	97	92	92	92	92	92	92	92	92
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97US-6667777.

11-APR-1997; 07-APR-1997; Α.

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Webber R;

WPI; 1998-594495/50.

Human iNOS peptide Human iNOS peptide Human iNOS peptide Rat inducible nitr Murine iNOS (1002- Inducible nitric o Ray iNOS (1006-102 Human iNOS peptide Amino acid sequenc Human endothelial Human endothelial Amino acid sequenc Human nitric oxide Endothelial nitrog	uman; immunoassay; detection; sepsis; septic shock; lupus; transplantation; psoriasis; ted".
15 19 AAM81255 15 19 AAM81312 15 19 AAM81312 114 1	ide; 18 AA.  ry)  ment PS-5185.  synthase; iNOS; h mic; quantitation; tissue rejection; tiple sclerosis.  r/Qualifiers  "Gln residue amida
882 884 881 881 881 881 881 882 884 883 884 883 884 883 884 883 884 883 884 883 884 883 884 883 884 883 884 885 886 886 887 887 887 887 887 887	81252 standar 81252; APR-1999 (fi an iNOS pepti ucible; nitri oclonal antib cardial infar oimmune disea o sapiens. ified-site 845710-A1. OCT-1998.
111 111 111 111 111 111 111 111 111 11	RESULT AAW81252 ID AAW8 XX AC AC XX DT 30-A XX DE HUMBI XX KW MODO KW KW KW MODO KW KW MODO KW KW KW MODO KW KW KW MODO KW KW KW KW MODO KW KW KW KW KW MODO KW KW KW KW KW MODO KW KW KW KW KW KW KW MODO KW KW KW KW KW KW MODO KW KW KW KW KW MODO KW KW KW KW KW MODO KW KW KW KW KW KW KW MODO KW KW KW KW KW KW KW KW MODO KW KW KW KW KW KW KW MODO KW KW KW KW KW KW KW KW MODO KW MOOO KW

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                                                                                                               This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.
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              Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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Pred. No. 1.7e-09;
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                                                                                 Example 4; Page 39; 93pp; English.
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Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                         18 AA;
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tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monoclonal antibody; mimić; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis; Mab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nitric oxide synthase; iNOS; human; immunoassay; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human iNOS peptide fragment capable of binding Mab 24B10-2C7.
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                                                                                                                                                                   100.0%; Score 97; DB 19;
100.0%; Pred. No. 1.7e-09;
Live 0; Mismatches 0;
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nes 18; Conser
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AAW81192

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Inhibition of cytokine mediated immunotoxicity of cells can be achieved by blocking free radical production or the accumulation of free radicals in that cell. Treatment of insulin dependent diabetes mellitus (IDDM) can be achieved by by blocking nitric oxide (NO) production in a pancreatic beta cell and by providing a composition comprising an agent that reduces levels of fatty acids in the cells and protects beta-cells of the subject against lipid-mediated cells and protects beta-cells of the subject against lipid-mediated cells can also be protected against nitric oxide mediated cytotoxicity by introducing into the cell an antioxidising agent. The methods can be used for protecting cells against immunotoxicity mediated by, e. g. IL-1 beta, IL-1 alpha, gamma IFN, IR-7 IL-1, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protection of mammalian cells against immunotoxicity or lipotoxicity - used for treating, e.g. diabetes, obesity, wasting syndromes, osteoporosis, inflammatory diseases, autoimmune diseases or
                                                                                                                     Manganese containing superoxide dismutase; MnSOD; IDDM; diabetes mellitus; treatment; therapy; nitrit oxide; No; beta cell; fatty acid; lipotoxic; cytotoxic; cytotine; osteoporosis; inflammatory disease; autofimmune disease; neurodegenerative disease.
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Pred. No. 1e-06;
0; Mismatches 1; Indels (
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, Thigpen A,
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                                                                          Inducible nitric oxide synthase.
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N-PSDB; AAX08434.
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    Inducible nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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Pred. No. 1.1e-08;
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      Human iNOS (1009-1026) peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW96322 standard; Protein; 1146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 21; 93pp; English.
                                                                                                                                                                                                                       AAW81192 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-6667777.
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94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US06500
                                              RMTLVFGSRRPDEDHIYQ 18
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Best Local Similarity 94.4
Matches 17; Conservative
  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WEBB/) WEBBER
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18;
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AAW96322 RESULT

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Human chondrocytes were incubated with interleukin-1-beta to induce nitric-oxide-synthase. CDNA was generated and used to construct a library in lambda ZAPII. This was screened with a 650 bp fragment of mouse inducible NO-synthase cDNA to identify the full-length clone pBSHSINOS. The insert was transferred to pSVL to give a vector capable of expressing NO-synthase in CHO cells under control of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An inducible nitric oxide syntase (1NOS = AAR88464) is the product
                                                                                                                                                                                                        for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inducible nitric oxide synthase; iNOS; hepatocyte; gene therapy; vascular occlusive disease; cancer; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inducible nitric oxide synthase gene - useful in gene therapy treat, e.g. vascular occlusive disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 15; Length 1153; 1e-06;
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                                                                                                                                                                                     New human inducible nitric oxide synthase - useful identifying enzyme inhibitors and stimulators, and and treatment of e.g. viral infections or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simmons RL,
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                                                                                                        Moncada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 92; DB 1
Pred. No. 1e-00
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatocyte inducible nitric oxide synthase.
                                                                                                       Palmer RMJ,
                                                                                                                                                                                                                                                            Disclosure; Page 25-31; 42pp; English
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                                                                                                                                                                                                                                                                                                                                                                                             heterologous constitutive promoter.
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   94WO-GB00621
                                   93GB-0006386
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                                                                 (WELL ) WELLCOME FOUND LTD
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYPI-) UNIV PITTSBURGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Geller DA,
                                                                                                       Charles IG, Moncada
                                                                                                                                        WPI; 1994-333198/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-068641/07.
                                                                                                                                                                                                                                                                                                                                                                                                                               1153 AA;
                                                                                                                                                      N-PSDB; AAQ77700
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   25-MAR-1994;
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                                   26-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ66914 is from human hepatocyte inducible nitric oxide synthase cDNA clone pHINOS from lambda Zap II CDNA library. The original source was induced human hepatocyte RNA. HINOS CDNA plasmid is pref. transformed in E. coli SOLK (ATCC 69126). The inventors claim a clone with the CDNA sequence in AAQ66914 and a CDNA clone which encodes AAR55764. The cloning and expression of a human tissue nitric oxide synthase CDNA provides a source of the enzyme for therapeutic purposes, for example to prevent the hypotensive shock seen with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                 Sequence encoded by the cDNA clone for human hepatocyte inducible nitric oxide synthase.
                                                                                                                                                                                                                                                                                                                                                                                                             WA clone encoding human inducible nitric oxide synthase - used prevent the hypotensive shock seen with sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor;
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                                                                                   Nitric oxide synthase; hepatocyte; hypotensive shock; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nitric-oxide-synthase; NO-synthase; NOS; chondrocyte; interleukin-1-beta; pBSHSTNOS; arthritis; hypertension; septic shock; inflammation; ischemia; dementia; obesity; agonist; antagonist; vector; CHO; Chinese hamster ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                             Simmons RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.8%; Score 92; DB 15; 94.4%; Pred. No. le-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 53pp; English.
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(first entry)
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                                                                                                                                                                                                                                                                                            PITTSBURGH
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                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-200273/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1153 AA;
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Matches 17; Conser
                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ66914
                                                                                                                                                                                                                                                                                            (UYPI-) UNIV
                                                                                                                      Homo sapiens
                                                                                                                                                                                                                        23-NOV-1993;
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                                                                                                                                                                                                                                                          25-NOV-1992;
28-DEC-1994
                                                                                                                                                     WO9412645-A.
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Sequence

sepsis.

CDNA

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                                                                                                                                                                                                 Gaps
of a cDNA clone (AAT10115) derived from human hepatocytes induced for INOS biosynthesis. The iNOS can be obtd. by expression of the cDNA e.g. in mammalian host cells and is used in the development of selective inhibitors of NOS or to treat diseases affected by nitric oxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment of erectile dysfunction - by introducing an agent into penile tissue, particularly for inducing cavernosal smooth muscle relaxation or increasing NOS levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erectile dysfunction; impotence; gene therapy; corpora cavernosa;
                                                                                                                                                                                               ;
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                                                                                                                                                           Score 92; DB 17; Length 1153;
Pred. No. 1e-06;
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nitric oxide synthetase; NOS; iNOS; HPiNOS; human;
                                                                                                                                                                                             1;
                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human inducible nitric oxide synthetase.
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                                                                                                                                                                                                                                                                                                                                                       AAW36113 standard; Protein; 1153 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rajfer J;
                                                                                                                                                           94.88;
94.48;
                                                                                                                                                                                                                                                    (GONZ/) GONZALEZ-CADAVID N F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0017373.
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                                                                                                                                                                                                                              1 RMTLVFGSRRPDEDHIYQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                           Ouery Match
Best Local Similarity 94.4
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-008577/01
                                                                                                          1153 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAJFER J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT98199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relaxant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid delivery vehicle comprising a nucleic acid encoding nitric oxide synthase, used for isolated tissue perfusion treatment to enhance and induce angiogenesis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a method for gene therapy for enhancing and inducing angiogenesis. The method uses a nucleic acid delivery vehicle, which comprises a nucleic acid encoding nitric oxide synthase (NOS). The delivery vehicle is used for the manufacture of a pharmaceutical composition for isolated tissue perfusion treatment. The method is useful for enhancing and/or inducing angiogenesis in patients with endothelial dysfunctions, in particular arteriosclerosis. The present sequence represents an inducible NOS.
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                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a human inducible nitric oxide synthase (NOS)
                                                                                                                                                                                                                                                                                                                                                                                                                             Gene therapy, angiogenesis; nucleic acid delivery; arteriosclerosis; nitric oxide synthase; NOS; endothelial dysfunction.
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Score 92; DB 19; Length 1153;
Pred. No. 1e-06;
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                                           1; Indels
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                                                Mismatches
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                                                                                                                                                                                                                                             AAB31724 standard; Protein; 1153 AA.
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                                                                                       1 RMTLVFGSRRPDEDHIYQ 18
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                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                           17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INTR-) INTROGENE BV.
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  Query Match
Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
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ID AAB6
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(WEBB/) WEBBER
                     07-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                  Use of a nucleic acid delivery vehicle comprising a nucleic acid encoding nitric oxide synthase, especially useful in gene therapy for enhancing and/or inducing anglogenesis and treating atherosclerosis \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vehicle comprising a nucleic acid encoding nitric oxide synthase (NOS) activity for the manufacture of a composition for essentially isolated tissue perfusion treatment to enhance and/or induce annylogenesis. The nucleic acid delivery vehicle is particularly useful in gene therapy for the treatment of atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to use of a nucleic acid delivery
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                                                                           NOS; anglogenesis; gene therapy.
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                                   Human inducible nitric oxide synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Examples; Page 14-18; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human iNOS peptide fragment PS-5283.
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94.4%;
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09-APR-2001 (first entry)
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Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                           Verlinden S;
                                                                       Nitric oxide synthase;
                                                                                                                                                                                                                                                                                                      (INTR-) INTROGENE BV
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Modified-site
                                                                                                                                                    EP1067190-A1
                                                                                                              Homo sapiens
                                                                                                                                                                                                                           09-JUL-1999;
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                                                                                                                                                                                       10-JAN-2001
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specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS potent in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autocimmune disease; multiple sclerosis; epitope mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes an immunoassay method where a sample with a
                                                                                                                                                                                                                                                          Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 39; 93pp; English.
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100.08; L.
27US-6667777
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                                                                                                                                                                                                     WPI; 1998-594495/50
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Matches 15; Conserv
                                                                   (WEBB/) WEBBER R.
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15-OCT-1998
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                                                                                                                                                                                                                   AAW81316
                                                                                                                                                                                                        RESULT
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                             This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNoS) or mimics of this protein is used to detect the presence of human iNoS protein in the sample. The method can be used for the detection and quantitation of human iNoS in cells and tissues for various pathophyslological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNoS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (inOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and
                                                                                                                                                                                                                                                                                                                                                                                                   Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes an immunoassay method where a sample with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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                                                                                                                                                                                           Length 15;
                                                                                                                                                                                                                Indels
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                                                                                                                                                                                           DB 19; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "His residue amidated"
                                                                                                                                                                                           84.5%; Score 82; DB 100.0%; Pred. No. 4.1
                                                                                                                                                                                                                                                                                                                                                                              Human iNOS peptide fragment PS-5287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 39; 93pp; English.
                                                                                                                                                                                                                                                                                                               AAW81259 standard; peptide; 15 AA
          Example 4; Fig 7D; 93pp; English.
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es 15; Conservative
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                                                                                                                                                            15 AA;
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                                                                                                                                        invention
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tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis; epitope mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nitric oxide synthase; iNOS; human; immunoassay; detection;
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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                                                                                                                                                                                                                                                                                           83.5%; Score 81; DB 19; I
100.0%; Pred. No. 5.9e-07;
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5.9e-07;
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RMTLVFGSRRPDEDH 15
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Search completed: September 10, 2001, 14:00:25 Job time: 169 sec

Perfect score:

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Scoring table: Sequence:

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093947 candida alb
014761 homo sapien
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A OGAWA Y., Nishijima S., Goto M., Ida M.;
Ogawa Y., Nishijima S., Goto M., Ida M.;
T "Cloning and characterization of a novel splice valiant of human
I inducible nitric oxide synthase.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB022318; BAA37123.1; -..
EMBL; AB022318; BAA37123.1; -..
Interpro; IPR001094; -..
Interpro; IPR001433; -..
Interpro; IPR001433; -..
Interpro; IPR001709; -..
R Interpro; IPR00175; Oxidored_fad; 1.
Pfam; PF0067; FAD_binding; 1.
Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00369; FAD_binding; 1.
R PRINTS; PR00371; FPNCR.
O SEQUENCE 1114 AA; 126748 MW; C1F9624774435571 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.5%; Score 86; DB 4; Length 1114; 94.4%; Pred. No. 7.4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
INDUCTBLE NITRIC OXIDE SYNTHASE.
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                                         090K99
099VLK8
099UL78
094404
044047
094FD3
099FP3
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098VA7
099XVA7
099XVA7
099XVA7
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098408
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096FT9
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SEQUENCE FROM N.A.
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094994
09r0w4 rattus norv 09qw28 rattus sp. 093865 candida alb 09229 saccharomyc P72704 synechocyst 09xwe0 caenorhabdi 09r116 acinetobact 09r310 acinetobact 074179 pleurotus o
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                                                                                                                                                  September 10, 2001, 14:11:14; Search time 72.54 Seconds (without alignments) 32.830 Million cell updates/sec
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0995v9 h
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                     425026 seqs, 132305027 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                OM protein - protein search, using sw model
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09R0W4
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P72704
Q9KWE0
Q9KWE0
Q9KR10
Q9K310
Q9K310
Q9Y5W9
Q9Y5W9
Q9Y5W9
Q9Y5W9
Q9Y5W9
Q9Y5W9
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_unclassified:*
sp_vertebrate:*
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Maximum DB seq length: 2000000000
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Database

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Gaps

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1 NNNVEKAPSATSSPVTQD 18

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homo sapien homo sapien homo sapien homo sapien

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Q9HFS7

Score

Result . 9 ~

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1147 AA; 130613 MW;
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Pfam: PF00667; FAD_binding; 1.
PRINTS: PR00369; FLAVODOXIN.
PRINTS: PR00371; FPNCR.
SEQUENCE 1147 AA; 130613 MW;
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PRINTS; PR00371; FPNCR.
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Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 74.7
Best Local Similarity 72.2
Matches 13; Conservative
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Interpro; IPR001709; -.
Interpro; IPR003097; -.
                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD001811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9QW28
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ACTION OF SEQUENCE FROM N.A.

A Kelnanen R.A., Vartiainen N., Kodstinabo J.;

B Kell., AJ230462; CAB46089.1; JOINED.

DR EMBL; AJ230465; CAB46089.1; JOINED.

DR EMBL; AJ230466; CAB46089.1; JOINED.

DR EMBL; AJ230470; CAB46089.1; JOINED.

DR EMBL; AJ230470; CAB46089.1; JOINED.

DR EMBL; AJ230471; CAB46089.1; JOINED.
                                                                                                                                                                                                                                                                                                                        MEDLINE:98431941; PubMed-9746458; Wang X., McGregor C.G.A., Miller V.M.; Wang X., McGregor C.G.A., Miller V.M.; Induction and cDNA sequence of inducible nitric oxide synthase from canine aortic smooth muscle cells."; Am. J. Physiol. 275:H1122-H1129(1998). EMBL; AF777821; AARC78630.1; -.. HISSP; P29477; INOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last sequence update)
1NDUCIBLE NITRIC OXIDE SYNTHASE.
Carls familiaris (Dog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 78.0%; Score 71; DB 6; Length 1154; Best Local Similarity 77.8%; Pred. No. 0.0023; Matches 14; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1154 AA; 131709 MW; 42CD606E447254CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INDUCIBLE NITRIC OXIDE SYMTHASE.
                            PRT; 1154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001094; -.
InterPro; IPR001033; -.
InterPro; IPR001433; -.
InterPro; IPR001709; -.
Pfam; PF00175; oxidored_fad; 1.
Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00363; FLAVODOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NNNVEKAPSATSSPVTQD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111111 | 11 | 11 | 12 | 25 NNNVEKPPGATPSPSTQD 42
                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       TISSUE: AORTA;
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Q9R0W4;
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109 PO

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MEDLINE-93221515; Pubmed-7682072;

MOOD E.R., Berger H.Jr., Sherman P.A., Lapetina E.G.;

Mood E.R., Berger H.Jr., Sherman P.A., Lapetina E.G.;

Mood E.R. and macrophages express an identical cytokine inducible an intric oxide synthase gene.";

I intric oxide synthase gene.";

Blochem. Biophys. Res. Commun. 191:767-774(1993).

R HSSP; P29477; INOS.

R InterPro; IPR001094; -...

R InterPro; IPR001433; -...

R InterPro; IPR001709; -...

R InterPro; IPR001709; -...

R InterPro; IPR001709; -...

R InterPro; IPR001709; -...

R Pfam; PF00175; Oxidored_fad; 1.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
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Pred. No. 0.0071;
0; Mismatches 5; Indels (
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1147 AA; 130625 MW; 2CAFB983E56F651A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E76B3F8407D54CF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
CYTOKINE INDUCIBLE NITRIC OXIDE SYNTHASE, INOS.
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EMBL, AJ230471, CAR46089.11, JOINED. EMBL, AJ230475, CAR46089.11, JOINED. EMBL, AJ230477, CAR46089.11, JOINED. EMBL, AJ230477, CAR46089.11, JOINED. EMBL, AJ230477, CAR46089.11, JOINED. EMBL, AJ230489, CAR46089.11, JOINED. EMBL, AJ230481, LORAGED. EMBL, AJ2446181, AJ230481, LORAGED. EMBL, AJ230481, LOR
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(ROTAMASE B).
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                                                                        P72704
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                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                             Leng P., Brown A.J.P.;
"The hyphal-specific gene ALS7 is a member of a Candida albicans gene family encoding agglutinin-like cell surface proteins.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF051313; AAD02580.1; ... C2327659AA911F2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                           Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54; DB 3;
Pred. No. 1.3;
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Pred. No. 14;
3; Mismatches
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                                                                                                                               1047 AA.
                                                                                                                                                                                                                          AGGLUTININ-LIKE CELL SURFACE PROTEIN
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                                                                                                                                 PRT;
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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.3%;
75.0%;
 18
                   25 NNNVEKTPGAIPSPTTQD 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0°
"Thea 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 59.3
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NNNVEKAPSATSSPVT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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309 NVQKVPSATNSKTTK 323
1 NNNVEKAPSATSSPVTQD
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ENCE 758 AA; 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purnelle B., Comblez
Submitted (JUN-1996)
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ATCC10261;
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5476;
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SEQUENCE
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01-JAN-1999 (TrEMBLrel. 09, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B (EC 5.2.1.8) (PPIASE B)
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-97061201: PubMed-8905231;

MEDLINE-97061201: PubMed-8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Miyajima N., Hirosawa M., Sugiura M., Nakazaki N., Naruo K., Okumura S.,

Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 3:109-136(1996).

-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.

-!- ENZYME REGULATION: INHIBITED BY CYCLOSPORIN A (CSA).

-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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"Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Isomerase; Rotamase.
SEQUENCE 246 AA; 26580 MW; 02080EE3C339932F CRC64;
                                                                                                                                                                                                                                                                           Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 AA
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                                                                                                                                                                                                                                                 Synechocystis sp. (strain PCC 6803)
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InterPro; IPR002130; -... PF00160; pro_isomerase; 2... PROSITE; PS00170; CSA_PPIASE_1; 1... PROSITE; PS50072; CSA_PPIASE_2; 1...
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PRELIMINARY;
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les 8; Conserv
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                                                                                                                                                                                                                                                                                 Bacteria; Cyanoba
NCBI_TaxID=1143;
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'PKLH1-like aberrant mercury resistance transposons of environmental
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Pred. No.
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6837 MW;
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Best Local Similarity 53.8
Fr. Conservative
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                                                                                                                                                                         2 NNVEKAPSATSSPVT 16
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Best Local Similaritý
Matches 8; Conserv
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                                                                                                   65 AA;
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SEQUENCE
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TRANSPOSON-ABERRANT MERCURY RESISTANCE TRANSPOSON;
Kholodii G.Y., Mindlin S.Z., Lomovskaya O.L., Gorlenko Z.M.,
Yurieva O.Y., Nikiforov V.G.;
"PKLH1-like aberrant mercury resistance transposons of environmental
Acinerobacter strains: spread, polymorphism and possible origin.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ251518; CAB65944.1; -.
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Kholodii G.Y., Mindlin S.Z., Lomovskaya O.L., Gorlenko Z.M.,
Yurieva O.V., Nikiforov V.G.;
                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pKLH103, Plasmid pKLH102, and Plasmid pKLH104.
Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
                                                                                          Length 305;
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Pred. No. 2.8;
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                                                            6D8A0D840B832416 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
URF-1 PROTEIN (FRAGMENT).
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Last annotation update)
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                                                                                         Score 46; DB 5;
Pred. No. 8.5;
4; Mismatches
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                                        InterPro; IPR002138; -. Pfam; PF00655; ICE_p10; 1. SEQUENCE 305 AA; 35084 MW;
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6837 MW;
        Science 282:2012-2018(1998).
EMBL; AL032657; CAA21735.2;
HSSP; P42574; 1CP3.
                                                                                         50.5%;
llarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                           Acinetobacter calcoaceticus.
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Best Local Similarity 53.3%;
Matches 8; Conservative
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investigating biology.";
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                                                                                                                                            : 1:1:1111
170 DPGPTASSSPLTQD 183
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                                                                                                                                 5 EKAPSATSSPVTQD 18
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                                      InterPro; IPR002138;
                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              65
65 AA;
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SEQUENCE
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Q9RHF6;
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Irie T., Honda Y., Matsuyama T., Watanabe T., Kuwahara M.;
"Genomic sequence encoding manganese peroxidase isozyme, MnP3 from the white-rot basidiomycete, Pleurotus ostreatus.";
submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB016519; BaA33009.2;
HSSP; P06181; 1B85
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
Acinetobacter strains: spread, polymorphism and possible origin."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ251340; CAB65956.1; -.
EMBL; AJ251338; CAB65948.1; -.
EMBL; AJ251338; CAB65952.1; -.
ProDom; PD003738; -; 1.
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Agaricales;
Pleurotaceae; Pleurotus.
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                                                                                                                                                                                                                                                                                   BF777CE1A70C4DB5 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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14;
                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 2;
Pred. No. 2.8;
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2; Mismatches
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PRINTS; PR00458; PREXXIDASE.
PROSITE; PS00435; PEROXIDASE.
PROSITE; PS00436; PEROXIDASE.2; UNKNOWN.1.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                        Nakamura Y.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
TAC and BAC clones.";
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MEDLINE-9919287; PubMed-10097140;
MISTAL Baffa R., Numata S.I., Murakumo Y., Rattan S., Inoue H.,
Ishii H., Baffa R., Numata S.I., Murakumo Y., Rattan S., Inoue H.,
Mori M., Fidanza V., Alder H., Croce C.M.;
"The FEXI gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors.";
Proc. Natl. Acad. Sci. U.S.A. 96:3928-3933(1999).
EMBL: ARI23656; AAD23837.1; -
SEQUENCE 504 AA; 55611 MW; 6665CACB72272BC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                            Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S., Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 26;
3; Mismatches 4; Indels
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SEQUENCE 652 AA; 73666 MW; D567964FFE1F4CE6 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
FEZI.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.5%;
                                                                                                                                                                                                                                                                                                                                    DNA Res. 7:217-221(2000).
EMBL; AP000371; BAB02532.1;
InterPro; IPR000313; -
InterPro; IPR001848; -.
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242 SNKADKGPSCVRSPISTD 259
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Best Local Similarity 56.29
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                                                 SEQUENCE FROM N.A.
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                           STRAIN-COLUMBIA;
PubMed-10907853;
                                                                          STRAIN-COLUMBIA;
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Q9Y5W0;
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09Y5V9
AC 09Y5V9
AC 09Y5V9, DT 01-NOV.
DT 01-NOV.
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CS FEZ
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Q9Y5W0
ID Q9Y5W0
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SEQUENCE FROM N.A.
MEDLINE-9919287; PubMed=10097140;
MEDLINE-9919287; PubMed=10097140;
Ishii H., Baffa R., Numata S.I., Murakumo Y., Rattan S., Inoue H.,
Mori M., Fidanza V., Alder H., Croce C.M.;
"The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors.";
and its expression is altered in multiple human tumors.";
Proc. Natl. Acad. Sci. U.S.A. 96:3928-3933(1999).
EMBL: AF123655; AAD23836.1; -.
SEQUENCE 537 AA; 59829 MW; CEOP771B162905IB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-9919287; PubMed=10097140; Murakumo Y., Rattan S., Inoue H., Ishii H., Baffa R., Numata S.I., Murakumo Y., Rattan S., Inoue H., Ishii H., Baffa R., Numata S.I., Murakumo Y., Rattan S., Inoue H., Mori M., Fidanza V., Alder H., Croce C.M.; "The FE21 gene at chromosome 8p22 encodes a leucine-zipper protein, and its expression is altered in multiple human tumors."; Proc. Natl. Acad. Sci. U.S.A. 96:3328-3933(1999).
EMBL; AF123657; AAD23838.1; - SEQUENCE 563 AA; 62910 MW; EGEFSD260E41380C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 31;
4; Mismatches 7; Indels
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Last annotation update)
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38.98;
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242 SNKADKGPSCVRSPISTD 259
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Matches 7; Conservative
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Best Local Similarity
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# GenCore version 4.5 Copyright (c) 1993 - 2000. Compugen Ltd.

OM protein - protein search, using sw model

September 10, 2001, 14:09:54; Search time 23.82 Seconds (without alignments) 25.886 Million cell updates/sec Run on:

US-08-833-506C-32 91 1 NNNVEKAPSATSSPVTQD 18 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 93435 seqs, 34255496 residues Searched:

93435

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cr	P35228 homo sapien	rattu	O60591 homo sapien	O46660 macaca mula	7 mus musc							Q89853 ebola virus	_		_					P32310 carassius a	escheric			ø		O61955 caenorhabdi	P40214 saccharomyc	e	ď			725	Q04893 saccharomyc
SUMMARIES	ID	NS2A_HUMAN	NOS2_RAT	NS2D_HUMAN	NOS2_MACMU	NOS2_MOUSE	ALS3_CANAL	MERE_PSEAE	HBL1_CAEEL	CEK1_SCHPO	TEGU_EBV	VGP_EBORE	VGP_EBORS	BRC2_MOUSE	LIN3_CAEEL	YS45_CAEEL	CC10_SCHPO	PME3_PHAVU	AMPN_RABIT	TSH_DROME	OPSB_CARAU	DAMX_ECOLI	GV7_XENLA	BRC1_DROME	BM88_PIG	F801_SCHMA	IFE3_CAEEL	YM22_YEAST	YIN5_YEAST	YFHA_ECOLI	AP54_YEAST	GUNB_CLOTM	TLE2_HUMAN	YM96_YEAST
	DB	-	Н	H	Н	Н	Н	Н	Н	-	-	٦	Н	П	Н	Н	٦	Н			Н									-1	Н	7	_	-
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P54683 dictyosteli	P34661 caenorhabdi	P72267 rhodococcus '	Q57060 haemophilus	_	Q09108 gallus gall		_	P32343 saccharomyc	Q95179 equus asinu	P20395 rattus norv	P47799 equus cabal
TAGB_DICDI	YOY3_CAEEL	TATA_RHOER	Y095_HAEIN	UPPS_CHLTR	SCF_CHICK	SP13_YEAST	GAT6_HUMAN	YKM4_YEAST	FSHR_EQUAS	FSHR_RAT	FSHR_HORSE
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1905	94	98	251	253	287	291	449	579	687	692	694
42.9	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8
39	38	38	38	38	38	38	38	38	38	38	38
					39						

## ALIGNMENTS

RESULT  NS2A_HUMAN  NS2A_HUMAN  NS2A_HUMAN  NS2A_HUMAN  DDT 01-FE  RESULT  RRY GELLE  RRY MEDLI  RR
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"Structural characterization of nitric oxide synthase isoforms reveals striking active-site conservation."; Nat. Struct. Biol. 6:233-242(1999).
-I- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RÁY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 74-504.
MEDITNE-99340067; Pubmed-10409685;
LLI H., Raman C.S., Glaser C.B., Blasko E., Young T.A., Parkinson J.F.,
Whitlow M., Poulos T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Crystal structures of zinc-free and -bound heme domain of human inducible nitric-oxide synthase. Implications for dimer stability and comparison with endothelial nitric-oxide synthase.";
J. Biol. Chem. 274:21276-21284(1999).
                                                                                                                                                                       Guo F.H., de Raeve R.H., Rice T.W., Stuehr D.J., Thunnissen F.B.J.M., Erzurum S.C.;
                                                                                                                                                                                                                                                                                           Luss H., Li R.-K., Shapiro R.A., Tzeng E., McGowan F.X., Yoneyama T., Hatakayama K., Geller D.A., Mickle D.A.G., Simmons R.L., Billiar T.R.;
                                                                                                                                                                                                   "Continuous nitric oxide synthesis by inducible nitric oxide synthase
                                                                                                                                                                                                                                                                                                                                                   ů
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BLOLLNE-96047340, PubMed-7558036;
Bloch KE-96047340, PubMed-7558036;
Bloch K-0. Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G., Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;
Trice members of the nitric oxide synthase II gene family (NOS2B, and NOSZC) colocalize to human chromosome 17.";
Genomics 27:526-530(1995).
                       SEQUENCE FROM N.A.
TISSUE-Glioblastoma;
MEDLINE-95155267; PubMed-7531687;
Hokari A., Zeniya M., Esumi H.;
Hokari d., Zeniya M., Esumi H.;
"Cloning and functional expression of human inducible nitric oxide synthase (NOS) cDNA from a glioblastoma cell line A-172.";
J., Blochem. 116:575-581(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                          McLay J.S., Chatterjee P., Nicolson A.G., Jardine A.G., McKay N.G. Ralston S.H., Grabowski P., Haites N.E., Macleod A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99173237; PubMed-10074942;
Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,
Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,
Weber P.C.;
                                                                                                                                                                                                                                                                                                                                 "Dedifferentiated human ventricular cardiac myocytes express inducible nitric oxide synthase mRNA but not protein in response IL-1, TNF, IFNgamma, and LPS.";
J. Mol. Cell. Cardiol. 29:1153-1165(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hawksworth G.M.;
"Nitric oxide production by human proximal tubular cells: a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taylor B.S., Alarcon L.H., Billiar T.R.; "Inducible nitric oxide synthase in the liver: regulation and
                                                                                                                                                                                                               in normal human airway epithelium in vivo.";
Proc. Natl. Acad. Sci. U.S.A. 92:7809-7813(1995).
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Biochem. Biophys. Res. Commun. 205:85-91(1994).
                                                                                                                                                                                                                                                                 TISSUE-Cardiac myocytes;
MEDLINE-97304504; PubMed-9160867;
                                                                                                                                SEQUENCE FROM N.A.
TISSUE-Airway epithelium;
MEDLINE-95372368; PubMed-7544004;
                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Kidney;
MEDLINE-95165725; PubMed-7532248;
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MEDLINE-98389865; Pubmed-9721329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunomodulatory mechanism?";
Kidney Int. 46:1043-1049(1994).
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 380-473 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function.";
Biokhimita 63:766-781(1998).
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--- ENZYME REGULATION REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST WITH MOUSE NOS2). ASPIRIN INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY SIMILARITY).

--- SUBGNIT: HOMODIMER.

--- SUBGNIT: HOMODIMER.

--- TISSUE SPECIFICITY: EXPRESSED IN THE LIVER, RETINA, BONE CELLS AND AIRMAY EPITHELIAL CELLS OF THE LUNG. NOT EXPRESSED IN THE NITRIC OXIDE + N NADP(+).
-1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.

CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) - CITRULLINE + PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNOR.
OXIGOTE GOVERNER:
Heme; Phosphorylation; Zinc; Metal-binding; Multigene family; (BY CAPK) (POTENTIAL).
(BY CAPK) (POTENTIAL).
(BY CAPK) (POTENTIAL). FMN (PYRIMIDINE PART) (BY SIMILARITY). FAD (ADP PART) (BY SIMILARITY). FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY). CALMODULIN-BINDING (POTENTIAL) -!- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES. 6 AND 4 ZINC.
PHOSPHORYLATION (
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D -> G (IN REF. 4 (IN REF. (IN REF. (IN REF. (IN REF. (IN REF. (IN REF. -!- SIMILARITY: BELONGS TO THE NOS FAMILY. マエアエエエスにの ^^^^^ ZINC EMBL, L09210; AAA59171.1; -EMBL, L24553; AAA36375.1; -EMBL, U73029; CAA51512.1; -EMBL, U05810; AAA56666.1; -EMBL, U1511; AAB50401.1; -EMBL, D26525; BAA05531.1; -EMBL, AP068236; AAC19133.1; -EMBL, S75615; AAA179.1; -EMBL, S75615; AAA179.1; -EMBL, S75615; AAA179.1; --Pfam; PF00667; FAD_binding; 1. Pfam; PF00175; oxidored_fad; 1. InterPro; IPR001433; -. InterPro; IPR001709; -. InterPro; IPR003097; -. InterPro; IPR001094; -. 1NSI; 07-JAN-00. 2NSI; 07-JAN-00. 4NOS; 04-FEB-00. 623 767 903 978 11076 1110 1115 234 578 423 439 608 676 800 200 23 154 177 PLATELETS 3D-structure 163730; CONFLICT CONFLICT CONFLICT CONFLICT MOD_RES NP_BIND NP_BIND NP_BIND METAL CONFLICT CONFLICT CONFLICT BINDING NP_BIND UP_BIND MOD_RES MOD_RES DOMAIN MIM;

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MEDLINE-93221515; PubMed-7682072;
Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
Hepatocytes and macrophages express an identical cytokine inducible nitric oxide synthase gene.";
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-WISTAR; TISSUE-Pancreatic islets;
MEDLIKE-95309542; PubMed=7540573;
Karlsen A.E., Andersen H.U., Vissing H., Larsen P.M., Fey S.J.,
Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,
Mandrup-Poulsen T., Boel E., Nerup J.;
"Cloning and expression of cytokine-inducible nitric oxide synthase
Diabetes 44:753-758(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                salea E., Reis D.J., Feinstein D.L.; **Cloning and expression of inducible nitric oxide synthase from rat
                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Vascular smooth muscle;

BEDILNE-29191721, Pubmed-7680561;
Nunokawa Y., Ishida N., Tanaba S.;
"Cloning of inducible nitric oxide synthase in rat vascular smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K., Kawasaki H., Sugimura T., Esumi H.; Molecular cloning of a cDNA encoding an inducible calmodulin-dependent nitric-oxide synthase from rat liver and its expression in COS 1 cells.";
                                                                                                                                                                                   O06518; P97774; O35765; O35766; Q64558; Q64005; Q63267; O1-JUN-1994 (Rel. 29, Created) O1-CT-1996 (Rel. 34, Last sequence update) O1-CCT-2000 (Rel. 34, Last sequence update) NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II) NOS.
                                                 ö
             Length 1153;
Score 86; DB 1; Length 112.
Pred. No. 6.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 191:767-774(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 191:89-94(1993).
                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SPRAGUE-DAWLEY; TISSUE-AStrocytes; MEDLINE-94231594; PubMed-7513765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SPRAGUE-DAWLEY; TISSUE-Aorta;
MEDLINE-94325351; Pubmed-7519448;
Geng Y.J., Almquist M., Hansson G.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Neurosci. Res. 37:406-414(1994).
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MEDLINE-94039059; PubMed-7693462;
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               94.58;
94.48;
                                                                                                25 NNNVEKAPCATSSPVTQD 42
                                                                               1 NNNVEKAPSATSSPVTQD 18
          Query Match
Best Local Similarity 94.4 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  muscle cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Michel T., Balligand J.-L.;
"Isolation and characterization of INOS from rat cardiocytes.";
submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
-| WITH DIVERSE FUNCTIONS TRROUGHOUT THE BODY.
-!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-DAHL/RAPP SALT SENSITIVE STRAIN; TISSUE-Vascular smooth muscle; MEDLINE-98195092; PubMed-9535415; Chen P.Y., Gladish R.D., Sanders P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NITRIC OXIDE + N NADP(+).
-!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBBUTE: HOMODIMER (BY SIMILARITY).

TISSUE SPECIFICITY: IN NORMAL KIDNEY, EXPRESSED PRIMARILY IN THE MEDULLARY THICK ASCENDING LIMB, WITH MINOR AMOUNTS IN THE MEDULLARY COLLECTING DUCT AND VASA RECTA BUNDLE.

INDUCTION: BY INTERFERENCY GAMMA AND LIPOPOLYSACCHARIDE.

SIMILARITY: BELONGS TO THE NOS FAMILY.
"cDNA cloning and expression of inducible nitric oxide synthase from rat vascular smooth muscle cells."; Biochim. Biophys. Acta 1218:421-424(1994).
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-97070590; PubMed-8913516;
Tsutsumishita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,
Futati S., Niwa M.;
Futati S., Niwa M.;
Sequence analysis of inducible nitric oxide synthase in rat kidney,
lung, and uterus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp salt-sensitive rats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASPIRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQÜENCE OF 509-740 FROM N.A.
STRAIN-WISTRA, TISSUE-Renal glomerulus;
STRAIN-WAISTRA, TISSUE-Renal glomerulus;
Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S.;
"Advances in the studies of NO synthesis regulation in mesanglial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Location of an inducible nitric oxide synthase mRNA in the normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morrissey J.J., McCracken R., Kaneto H., Vehaskari M., Montani D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN.
                                                                                                                  H., Aoyama
                                                                                                             Kosuga K., Yui Y., Hattori R., Sase K., Eizawa H., Aoyam
Inoue R., Sasayama S.;
"Cloning of an inducible nitric oxide synthase from rat
polymorphonuclear neutrophils.";
Endothelium 2:217-221(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SPRAGUE-DAWLEY; TISSUE=Renal glomerulus; MEDLINE=94276509; PubMed=7516453;
                                                                                                                                                                                                                                                                                                                                                                      Biol. Pharm. Bull. 19:1374-1376(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypertension 31:918-924(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kidney Int. 45:998-1005(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 420-479 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nefrologia 16:35-39(1996).
                                                                                           SEQUENCE FROM N.A.
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25 NNNVEKTPGAIPSPTTQD 42

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                                                                                                                                                                                                               Oxidoreductase; naur, enc.

Zinc; Metal-binding; Multigene family.

BINDING 197 197 HEME (BY SIMILABITY).

DOMAIN 506 526 CALMODULIN-BINDING (POTENTIAL).

NP_BIND 620 651 FWN (PYRIMIDINE PART) (BY SIMILARITY).

NP_BIND 764 775 FAD (ADP PART) (BY SIMILARITY).

NP_BIND 975 993 NADP (RIBOSE PART) (BY SIMILARITY).

NP_BIND 975 993 NADP (RIBOSE PART) (BY SIMILARITY).

NP_BIND 1073 1088 NADP (ADP PART) (BY SIMILARITY).

METAL 107 107 ZINC (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1147;
                                                                                                                                        InterPro; IPR001034; ...
InterPro; IPR001433; ...
InterPro; IPR001433; ...
InterPro; IPR001095; ...
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                         7 AND 8).
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D -> G (IN REF. 10).
ET -> VP (IN REF. 1)
Q -> P (IN REF. 10).
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(IN REF. 3).
(IN REF. 3).
(IN REF. 8).
(IN REF. 8).
(IN REF. 8).
(IN REF. 3).
(IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 68; DB 1;
Pred. No. 0.0048;
); Mismatches :
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                PONSHRERHASCIA
                                                                                                                                                                                                                                                                                                        ^ ^ ^ ^ ^ ^ ^ ^ ^ ^
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                                        D12520; BAA02090.1;
L12562, AAA41720.1;
X76811; CAA54208.1;
D44591; BAA07994.1;
B98561; BAA12035.1;
AF006619; AAC16401.1;
AF006619; AAC16401.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                  EMBL; U48829; AAB18620.1; -. EMBL; S71597; AAB31028.2; -. EMBL; L36063; AAC02242.1; -. PIR; JC1472; JC1472.
                EMBL; D14051; BAA03138.1; -. EMBL; U26686; AAA85861.1; -.
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72.28;
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412
477
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Best Local Similarity
                                                                                                                                    HSSP; P29477; 1NOC
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EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
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NESTOLIUMAN

1D 882D-HUMAN

1D 0847-2000 (Red. 39, Created)

1D 0447-2000 (Red. 39, Created)

1D 0447-2000 (Red. 40, Last sequence update)

1D 0447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOI. Med. 2:27-37(1996).
-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. INOS AND NO MAY CONTRIBUTE TO SIMIAN IMMUNODEFICIENCY VIRUS (SIV)-INDUCED CENTRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NERVOUS SYSTEM DISEASE.

CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE + NITRIC OXIDE + N NADP(+).
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lane T.E., Buchmeler M.J., Watry D.D., Fox H.S.; "Expression of inflammatory cytokines and inducible nitric oxide synthase in brains of SIV-infected rhesus monkeys: applications to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
(INDUCIBLE NOS) (INOS) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE ENZYME (BY SIMILARITY).
-i- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY
                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                       Length 1147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme; Multigene family.
                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                        FF7E4C7ABA76D820 CRC64;
N -> S (IN AAC83554).
G -> A (IN AAC83554).
G -> E (IN AAC83554).
P -> Q (IN AAC83554).
H -> N (IN AAC83554).
TL -> NF (IN AAC83554).
TL -> NF (IN AAC83554).
I -> L (IN AAC83554).
F -> Y (IN AAC83554).
                                                                                                                                                                                                    Score 68; DB 1;
Pred. No. 0.0048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV-induced central nervous system disease.";
                                                                                                                                                                                                                                                                                                                                                                               162 AA.

    -i- INDUCTION: BY LIPOPOLYSACCHARIDES.
    -i- SIMILARITY: BELONGS TO THE NOS FAMILY.

                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Microglia;
MEDLINE-97056192; PubMed-8900532;
                                                                                                                                                          MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca mulatta (Rhesus macaque).
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72.28;
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                                                                                                                                                        AA; 130528
                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                                    25 NNNVEKTPGAIPSPTTOD 42
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                   1 NNNVEKAPSATSSPVTQD
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                                                               731
937
1009
1024
1076
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                                                                                                                                                                                    Ouery Match
Best Local Similarity
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                                                             731
937
1008
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046660;
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE-92357701; PubMed-1379716;
Lowenstein C.J., Glatt C.S., Bredt D.S., Snyder S.H.;
"Cloned and expressed macrophage nitric oxide synthase contrasts with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-DBA/23, BALB/CBY3, SJL/J, NOD/LTJ, AND B10.S/J; TISSUE-Spleen; Ma R.2., Teuscher C.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97477482; PubMed-9334294;
Crane B.R., Arvai A.S., Gachhui R., Wu C., Ghosh D.K., Getzoff E.D.,
Stuchr D.J., Tainer J.A.:
"The structure of nitric oxide synthase oxygenase domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92210618; PubMed-1372907;
Lyons C.R., Orloff G.J., Cunningham J.M.;
"Molecular cloning and functional expression of an inducible nitric
oxide synthase from a mutrine macrophage cell line.";
J. Biol. Chem. 267:6370-6374(1992).
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kone B.C., Schwoebel J., Turner P., Mohaupt M.G., Cangro C.B.; "Role of NF-kappa B in the regulation of inducible nitric oxide synthase in an MTAL cell line.";
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P29477; O70515; O70516;
01-APR-1993 (Rel. 25, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE (INDUCIBLE NOS) (INOS) (MAC-NOS).
                                                                             Score 65; DB 1; Length 162;
Pred. No. 0.0016;
                                                                                                           . 3; Indels
                             0457464D32287065 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).
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MEDLINE-20031637; PubMed-10562538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 116-496.
                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Am. J. Physiol. 269:F718-F729(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96088781; PubMed=7503239;
           162
17813 MW;
                                                                             71.48;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibitor complexes.";
Science 278:425-431(1997).
                                                                                                                                           1 NNNVEKAPSATSSPVTQD 18
                                                                                                                                                             Science 256:225-228(1992).
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                      (Mouse)
   1
162
162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the brain enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                            Similarity
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).

-1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO MEDIAPES TUNORICIDAL ACTIONS.

-1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE + NITRIC OXIDE + N NADPH+).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN HINHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY.
Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhul R., Crooks C., Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.; "Inducible nitric oxide synthase: role of the N-terminal beta-hairpin hook and pterin-binding segment in dimerization and tetrahydrobiopterin interaction."; EMBO J. 18:6260-6270(1999).
                                                                                                                                                                                                                                                                                                                                                                                  Amin A.R., Vyass P., Attur M., Leszczynska-Piziak J., Patel I.R., Welssmann G., Abramson S.B.; "The mode of action of aspirin-like drugs: effect on inducible nitric oxide synthase.";
                                                                                                    X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.
MEDLINE-98182450; PubMed-9516116;
Crane B.R., Arval A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                          Structure of nitric oxide synthase oxygenase dimer with pterin and ubstrate ^{\prime\prime}:
                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.
MEDLINE-20031638; PubMed-10562539;
Cane B.N.; Rosenfeld R.J., Arval A.S., Ghosh D.K., Ghosh S.,
Tainer J.A., Stuehr D.J., Getzoff E.D.;
"N-terminal domain swapping and metal ion binding in nitric oxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBUNIT: HOMODIMER.
-1- TISSUE SPECIFICITY: MACROPHAGES.
-1- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES.
-1- SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF065921; AAC17916.2; -. AF065922; AAC17917.1; ALT_INIT. AF065923; AAC17918.2; -.
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M84373; AAA39834.1; -
U43428; AAC52356.1; -
AF065919; AAC17914.1; -.
AF065920; AAC17915.1; -.
                                                                                                                                                                                                                                                                                                                                                         TISSUE-Macrophage;
MEDLINE-95372392; PubMed-7544010;
                                                                                                                                                                                           Science 279:2121-2126(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M87039; AAA39315.1; -.
                                                                                                                                                                                                                                                                                                                 EMBO J. 18:6271-6281(1999).
                                                                                                                                                                                                                                                                                                    synthase dimerization.
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23-MAR-99.
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LNOS; 18-NOV-98.
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A42166; A42166.
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                                                                                                                                                                                                                                                                                                                                            EFFECT OF ASPIRIN.
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                                                                                                                                                    Painer J.A.;
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2NOS;
1NOD;
2NOD;
3NOD;
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PDB;
PDB;
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PIR;
PDB;
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                                                                                                                                                                                                                                                                                                          CALMODULIN-BINDING (POTENTIAL).
FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoyer L.L., Payne T.L., Bell M., Myers A.M., Scherer S.; "Candida albicans ALS3 and insights into the nature of the ALS gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida. NCBL_TaxID=5476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family.";
Curr. Genet. 33:451-459(1998).
-!- FUNCTION: MAY PLAY A ROLE IN ADHESION AND PATHOGENESIS.
-!- FUNCTION: MAY PLAY A ROLE IN ADHESION AND PATHOGENESIS.
-!- PTM: N-GLYCOSYLATED AND O-GLYCOSYLATED (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57; DB 1; Length 1144; Pred, No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                N STRAIN NOD/LTJ).
N STRAIN SJL/J).
N STRAIN BALB/CBYJ).
                                                                                                                                                                                                                                                                                                                                                                                                                                               C -> R (IN STRAIN NOD/LFJ).
P -> L (IN STRAIN SJL/J).
S -> E (IN STRAIN BALB/CBVJ).
K -> T (IN REF. 4).
A -> V (IN REF. 2).
A -> G (IN REF. 2).
A MW, 0735BE676I13457F CRC64;
                                                                                                                                                                                                                                                         Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme; Zinc; Metal-binding; Multigene family; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
AGGLUTININ-LIKE PROTEIN 3 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1119 AA
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                                                                                                                                                                                                                                                                                               HEME.
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                                                                                                                                    Interpro; IPR001433; -.
Interpro; IPR001709; -.
Interpro; IPR003097; -.
Pfam: PF00667; FAD_binding; 1.
Pfam; PF00175; oxidored_fad; 1.
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61.1%;
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Best Local Similarity 61.17
Matches 11; Conservative
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990
1085
104
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967
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Interpro; IPR001094;
                                                  1DWX; 06-FEB-00.
1QOM; 15-DEC-99.
1DD7; 29-MAR-00.
08-DEC-99.
04-FEB-00.
06-FEB-00.
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074623;
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Plasmid.
SEQUENCE
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HBL1_CAEEL
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or send an email to license@isb-sib.ch).
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Brown N.L., Misra T.K., Winnie J.W., Schmidt A., Sieff M., Silver S.,
"The nucleotide sequence of the mercuric resistance operons of
plasmid R100 and transposon Th501: further evidence for mer genes
which enhance the activity of the mercuric ion detoxification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                        AGGLUTININ-LIKE PROTEIN 3.
10 X 36 AA TANDEM REPEATS.
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01-JAN-1988 (Rel. 06, Last sequence update)
01-CT-1989 (Rel. 12, Last annotation update)
HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERE.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC
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                                                             Repeat; Signal
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                                                                             POTENTIAL.
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                                                             Cell adhesion; Glycoprotein;
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75.0%;
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Best Local Similarity 75.0
Matches 12; Conservative
                                            EMBL; U87956; AAC39486.1;
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P06690;
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-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-!- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN ECTODERMAL CELLS DURING EMBRYONIC AND LARVAL DEVELOPMENT.
-!- SIMILARITY: BELONGS TO THE HUNCHBACK FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=99117349; PubMed=9917360;
Fay D.S., Stanley H.M., Han M., Wood W.B.;
Fay D.S., Stanley H.M., Han M., Wood W.B.;
Fay denorhabditis elegans homologue of hunchback is required for late stages of development but not early embryonic patterning.";
Dev. Biol. 205:240-253(1999).
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Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 78;
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E1EF23E690CF115D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB 1;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HBL1_CAEEL STANDARD; PRT; 982 AA. 09XYD3; 019389; 01-0CT-2000 (Rel. 40, Created) 01-0CT-2000 (Rel. 40, Last sequence update) 01-0CT-2000 (Rel. 40, Last annotation update) HUNCHBACK-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00096; zf-C2H2; 9.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
system.";
Mol. Gen. Genet. 202:143-151(1986).
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WormPep; F13D11.2; CE23646.
InterPro; IPR000822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8410 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF097737; AAD16170.1;
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 200027; CAA77325.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 | |: || |: || 2 NNPERLPSETHKPIT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NNVEKAPSATSSPVT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HBL-1 OR F13D11.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
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TEGU_EBV
P03186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEGU_EBV
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                                                                                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                           Gaps
  ZINC_FINGER_C2H2_2; 4.
ein; Gap; Zinc-finger; Metal-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Samejima I., Yanagida M.; Indactification of cut8+ and cek1+, a novel protein kinase gene, and complement a fission yeast mutation that blocks anaphase."; Mol. Cell. Biol. 14:6361-6371(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyne M., Rajandream M.A., Barrell B.G., Volckaert G.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY FACILITATE THE PROGRESSION OF ANAPHASE THROUGH
DIRECT OR INDIRECT INTERACTION WITH THE CUTB PROTEIN.
-!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
PROTEIN KINASES. STRONG, TO YEAST RIMIS.
                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                  1; Length 982,
                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                      49812554CF3CE30F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CEKI_SCHPO STANDARD; PRT; 1338 AA. P88938 , O9Y7N8; O1-EB-1995 (Rel. 40, Last sequence update) O1-OCT-2000 (Rel. 40, Last sequence update) O1-OCT-2000 (Rel. 40, Last annotation update) PROTEIN KINASE CEKI (EC 2.7.1.-). Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                    48.4%; Score 44; DB 55.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                       C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
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Mol. Cell. Biol. 14:7683-7683(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-94344146; PubMed-8065367;
                                                                                                                                                                                                                                          106951 MW;
                                                                                                                                                                                                                                                                                                                                                                                                      289 NNNNEEAPASTVSACSTPTT 308
                                                                                                                                                                                                                                                                                                                                                                                16
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                                                                                                                                                                                                                                                                                                                                                                              1 NNNVEKAP----SATSSPVT
                                                                                                                                                                                                                                                                                                  Query Match 48.4
Best Local Similarity 55.0
Matches 11; Conservative
                                         protein.
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InterPro; IPR000719; -.
InterPro; IPR000961; -.
InterPro; IPR002290; -.
                                                             358
384
560
589
617
756
951
PS50157; ZINC_
ental protein;
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NCBI_TaxID=4896;
                                                                                                                                                                                                                   957
982 AA;
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                                         Nuclear
                                                             336
361
567
567
563
623
929
                        Developmental
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SEQUENCE
                                       Repeat;
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ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
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ZN_FING
    PROSITE;
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        PFGMI;
        PF00069;
        pkinase;
        2.

        PROMITE;
        PS00107;
        PROTEIN_KINASE_ATP;
        FALSE_NEG.

        PROSITE;
        PS00108;
        PROTEIN_KINASE_DOM;
        1.

        PROSITE;
        PS500119;
        PROTEIN_KINASE_DOM;
        1.

        Transferase;
        Serine/threonine-protein
        kinase;
        ATP-binding.

        DOMAIN
        598
        PROTEIN KINASE.
        N.

        NP_BIND
        595
        603
        ATP (BY SIMILARITY).

        BINDING
        618
        618
        ATP (BY SIMILARITY).

        ACT_SITE
        713
        713
        BY SIMILARITY).

        ACT_SITE
        713
        BY SIMILARITY.
        S-> VCHIRGROLHSD (NR PERCENTEDONELLESCLRKLDVWH SCONELLY).

        SEQUENCE
        1338
        AA;
        149896
        MW;
        755DD0A13D3D2762
        CRC64;

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                                                                                                                                                                                                                                                                                                                                                                                                      Length 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
NCBI_TaxID=10377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3149 AA; 337954 MW; 3DD0C576587313D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 1;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 1;
Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 01, Last sequence update) (Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 3149 AA.
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(Rel. 01, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                         48.48;
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Best Local Similarity 44...
Best Conservative
                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 43...
T; Conservative
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814 NSAEDSPTATNTPTSQ 829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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21-JUL-1986
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us-08-833-506c-32.rsp

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CARBOHYD
                                                                                                                                                                                                    RESULT 12
                                                                                                              Matches
                                                                                                                                                                                                                VGP_EBORS
  FFFF8
                                                                                                                                                              Dp
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
L. Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
.. IS RESPONSTBLE FOR BINDING TO TARGET CELLS AND SUBSEQUENT FUSION
SC OF THE VIRAL AND HOST-CELL MEMBRANES
.. OF THE VIRAL AND HOST-CELL MEMBRANES
.. SUBUNIT: HOMOTRIMER; EACH MONOMER CONSIST OF A GP1 AND A GP2
SUBUNIT: HOMOTRIMER; EACH MONOMER CONSIST OF A GP1 AND A GP2
.. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. GP1 CAN ALSO BE
SHED BY THE VIRUS AFTER PROTEOLYTIC PROCESSING (BY SIMILARITY).
.. SUBCELLULAR LOCATION: TYPE I ALSO BE O-GINCOSTING (BY SIMILARITY).
.. SUBCELLULAR LOCATION GP1 AND GP2 IS EFFECTED BY THE HOST FURIN (BY SIMILARITY).
.. STANSCELLANEOUS: THE FULL-LENGTH GLYCOPROTEIN IS SYNTHESIZED AS A RESULT OF RNA EDITING, AN ADDITIONAL A RESIDUE IS INSERTED DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                               Sanchez A., Trappier S.G., Mahy B.W.J., Peters C.J., Nichol S.T.; "The virion dyroporteins of Ebola viruses are encoded in two reading frames and are expressed through transcriptional editing."; Proc. Natl. Acad. Sci. 0.5.A. 93:3602-3607(1996).
                                                                                                             Ebola virus (strain Reston) (Ebo).
Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Envelope protein; Glycoprotein; Signal; RNA editing SIGNAL 1 32 POTENTIAL.
CHAIN 33 677 STRUCTURAL GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 40, Last annotation update)
STRUCTURAL GLYCOPROFIN PRECURSOR (VIRION SPIKE GLYCOPROFEIN)
[CONTAINS: GP1; GP2].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .)
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              677 AA
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              PRT:
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EMBL; AF034645; AAC24346.1; -.
InterPro; IPR002561; -.
Pfam; PF01611; Filo_glycop; 1.
              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502
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673
677
609
                                                                                                                                              NCBI_TaxID=129003;
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
            VGP_EBORE
Q66799;
                                                                                                                                     Filovirus.
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TRANSMEM
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DISULFID
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MEDLINE—96195018; Pubbmed=8622982;
A Sanchez A., Trappier S.G., Mahy B.W.J., Peters C.J., Nichol S.T.;
Sanchez A., Trappier S.G., Mahy B.W.J., Peters C.J., Nichol S.T.;
The virion glycoproteins of Ebola viruses are encoded in two reading
frames and are expressed through transcriptional editing.";
Proc. Natl. Acad. Sci. U.S.A. 93:3602-3607(1996).
I. Proc. Natl. Acad. Sci. U.S.A. 93:3602-3607(1996).
I. PREPONSTBLE PROTEIN THAFF FORMS THE VIRION SPIKE AND WHICH
IS RESPONSTBLE FOR BINDING TO TARGET CELLS AND SUBSEQUENT FUSION
OF THE VIRAL AND HOST-CELL MEMBRANES.
C. SUBUNIT HONGTRIBER, EACH MONOMER CONSISTS OF A GP1 AND A GP2
SUBUNIT LINKED BY DISCUFIDE BONDS (BY SIMILARITY).
C. SUBUNIT LINKED BY DISCUFIDE BONDS (BY SIMILARITY).
C. SUBURIT LINKED BY COULD ALSO BE O-GLYCOSYLATED (BY SIMILARITY).
C. SUBURIT LINKED STORED AND GP2 IS EFFECTED BY THE HOST FUNIN (BY SIMILARITY).
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Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
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30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
STRUCTURAL GLYCOPROFEIN PRECURSOR (VIRION SPIKE GLYCOPROTEIN)
[CONTAINS: GP1; GP2].
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MEDLINE-97/S4941; PubMed-9242436;
MEDLINE-97/S4941; PubMed-9242436;
MCALLISTER K.A., Haugen Strano A., Hagevik S., Brownlee H.A.,
Collins N.K., Futreal P.A., Bennett L.M., Wiseman R.W.;
"Characterization of the rat and mouse homologues of the BRCA2 breast
cancer susceptibility gene.";
Cancer susceptibility gene.";
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MEDLINE-97075121; PubMed-8917547;
Rajan J.V., Wang M., Marquis S.T., Chodosh L.A.;
"Brcaz is coordinately regulated with Brcal during proliferation and differentiation in mammary epithelial cells.";
Proc. Natl. Acad. Sci. U.S.A. 93:13078-13083(1996).
                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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Sharan S.K., Bradley A.;
"Murine Brca2: sequence, map position, and expression pattern.";
Genomics 40:234-241(1997).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilensib.ch).
[5]
SEQUENCE OF 569-625 FROM N.A.
MEDLINE-97341126; PubMed-9196008;
MCAllister K.A., Ramachandran S., Haugen-Strano A., Fiedorek F.T. Jr.,
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PROSITE; PS50138; BRCA2_REPEAT; 6.
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EMBL, U72947; AAB40720.1; -.
EMBL, U65594, AAC23702.1; -.
EMBL, U89652; AAB71377.1; -.
EMBL, U89503, AAC53276.1; -.
MGD, MGI:109337; Brca2.
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YS45_CAEEL
Q09660;
                                                        DISULFID
DISULFID
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CARBOHYD
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CONFLICT
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YS45_CAEEL
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                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-92350298; PubMed-1641037;
Hill R.J., Sternberg P.W.;
"The gene lin-3 encodes an inductive signal for vulval development in
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
K -> E (IN STRAIN C57BL/6).
T -> S (IN STRAIN C57BL/6).
DSPKW -> SQSQV (IN STRAIN C57BL/6).
A -> G (IN STRAIN 129/SV).
E -> K (IN STRAIN 129/SV).
PR -> P (IN STRAIN 129/SV).
R -> K (IN STRAIN 129/SV).
R -> K (IN STRAIN 129/SV).
                                                                                                                5;
                                                                                             Score 43.5; DB 1; Length 3329;
Pred. No. 1.3e+02;
2; Mismatches 4; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mormpep, 736H1.4; CE18670.
InterPro; IPR000561; -
PR051TE; PS00122; EGF_1: 1.
PR051TE; ES01186; EGF_2: 1.
EGF-like domain; Growth factor; Transmembrane; Signal;
                                                                                                                                                                                                                    01-0cT-1993 (Rel. 27, Created)
01-0cT-1993 (Rel. 27, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X68070; CAA48207.1; -.
EMBL; Z68760; CAA92997.1; -.
EMBL; AL032641; CAA92997.1; JOINED.
EMBL; AL032641; CAA21649.1; -.
EMBL; Z68760; CAA21649.1; JOINED.
PIR; S28263; S28263.
                                                                                                                                            1604 NNVEKNPRICCICQSSYPVTED 1625
                                                                                                                                  2 NNVEKAP----SATSSPVTQD 18
3081
3089
3109
3220
3238
3243
3245
3245
                                                                                             47.8%;
                                                                                                                                                                                                                                                          LIN-3 OR LET-94 OR F36H1.4. Caenorhabditis elegans.
                                                                                           Query Match 47.8%
Best Local Similarity 50.0%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                  C. elegans.";
Nature 358:470-476(1992).
                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                  LIN-3 PROTEIN PRECURSOR
3081 3083
3089 3089
3105 320
3220 3220
3242 3242
3242 3245
3245 3245
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                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                       LIN3_CAEEL
ID LIN3_CAEEL
AC Q03345;
                                                                  SEQUENCE
                  VARIANT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMILTED (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL).
EGF-LIKE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
MISSING (IN REF. 2).
MISSING (IN REF. 2).
MISSING (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U21321; AAB36969.1; -.
WORDREP; ZK177.5; CE02094.
InterPor, IPR001128; -.
PROSITE; PS00086; CYTOCHRONE_P450; 1.
PROSITE; PS00086; CYTOCHRONE_P450; 1.
BINDING HENDE (BY SIMILARITY).
SEQUENCE 428 AA; 49015 MW; 71DFB8BB35FIEE7A1 CRC64;
                                                                                                                                                                                                                                                                                              Score 42; DB 1; Length 438;
Pred. No. 23;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                    LIN-3 PROTEIN.
EXTRACELLULAR (POTENTIAL).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PUTATIVE CYTOCHROME P450 CYP44 (EC 1.14.--).
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428 AA
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0; Mismatches
    POTENTIAL.
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Best Local Similarity 73.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                             2 NNVEKAPSATSSPVT 16
                                                                                                                                                                                                                                                                                                                                                                                                                  77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 NVEKCPYSPTSSPNT
                                                                                                                                                                                                                                                                                                                                                                                                                    63 NEIGDAPSSTSTPET
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
    1
14
14
231
254
150
150
1184
161
161
111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson K.;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 10, 2001, 14:01:15; Search time 42.28 Seconds (without alignments) 32.430 Million cell updates/sec Run on:

1 NNNVEKAPSATSSPVTQD 18 US-08-833-506C-32 91 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	576 nitric-oxide synth	nitric-oxide	hypothetical			hypothetical	hunchback-rel		38 BPLF1 protein - hu		No breast cancer susc					lin-3 protein	hypothetical p	hypothetical	cdc10 start c	200 C = 100 C								
0,	ID	A4967	S47647	15657	\$38253	I531	JC5(	JC5028	JC5029	A432	S654	865169	8745	T269	T16057	T436	T40993	OOBE	T30835	T42205	T30904	A75169	T41119	T24546	S28263	T20772	T27763	COZPCD	305170
	DB	7	-					7																					Ī
	Length		1147	1147	1147	1147	1147	1147	1147	1144	1147	758	246	394	806	982	1338	3149	3328	3329	3329	349	1045	366	438	639	428	767	226
æ	Query	94.5	74.7	74.7	74.7	74.7	74.7	74.7	74.7	62.6	60.4			50.5	48.4	48.4	48.4		47.8					46.2		46.2	45.6	45.6	1 2 7
	Score	98	68	68	68	89	99	89	68	57	22	47	46			44	44	44	•	43.5	•	43	43		42	42	;	41.5	
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a)	hypothetical prote	hypothetical prote	hypothetical prote	Hsk1 protein kinas	pectinesterase pre	probable transcrip	hypothetical prote	probable tron-sulf	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	NADH dehydrogenase	probable homeotic	merE protein - Xan
844995	T45818	T28025	T31706	T43513	S53105	T18233	T20785	C75259	T21676	T20771	T20774	T29612	D81219	A38437	870148
7	7	~	~	7	7	7	~	7	~	7	~	~	7	7	7
347	474	492	509	545	581	662	1011	1132	2586	4549	4667	727	753	993	78
45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	44.5	44.5	44.5	44.0
41	41	41	41	41	41	41	41	41	41	41	41	40.5	40.5	40.5	40
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT.  A49507  Intricrocated synthase (EC 1.14.13.39), inducible - human  C.Species: Homo saptens (most puens (most synthase)  C.Dates: 1-Fab-1996 issequence_revision ic-Fab-1996 iteta.Change 20-Jun-2000  C.Accession: A495076; XX0345, G01447; 138933; S47566; A47415  F.Charles: I.G.; Pamer. R. M.; Hickery, M. S.; Bayliss, M.T.; Chubb, A.P.; Hall, V.S.;  P.CC. NALL. Acad. Scil. U.S. A. 90, 11419-11423, 1993  A.Accession: A49506  A.Stetus: preliminary  A.Residues: 1-1153 < RES.  A.Cross references: BMEL.730029; NID:9441452; PIDN:CAA51512.1; PID:9441453  A.Title: Cloning and functional expression of human inducible nitric oxide synthase (A. A. A
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Gaps

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Indels

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C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C;Accession: 156575
B;Galea, E.; Reis, D.J.; Feinstein, D.L.
J. Neurosci. Res. 37, 406-414, 1994
A;Title: Cloning and expression of inducible nitric oxide synthase from rat astrocyte A;Reference number: 156575; MUID:94231594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Wolecule type: mRNA
A; Residues: 1-1147 <ADA>
A; Residues: 1-1147 <ADA>
A; Residues: 1-1147 <ADA>
A; Experimental source: GB:D12520; NID:g391858; PIDN:BAA02090.1; PID:g391859
A; Experimental source: liver
B; Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.
Biochem. Blophys. Res. Commun. 191, 767-774, 1993
A; Title: Hepatocytes and macrophages express an identical cytokine inducible nitric on A; Reference number: JN0457; MUID:93221515
A; Reference number: JN0457
A; Accession: JN0457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NAD C; Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein re C; Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me F; 536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Molecular cloning of a cDNA encoding an inducible calmodulin-dependent nitri
A;Reference number: S38253; MUID:94039059
A;Accession: S38253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-41,'SS',44-103,105-190,'Q',192-213,'R',215-247,'T',249-263,'I',265-373,
'S',896-1000,'LG',1003-1015,'RR',1018-1026,'EQ',1029-1147 <WOO>
A;CrossIreferences: PIDN:AAB26037.1
A;Experimental source: liver
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H.; Suzuki, H.; Nagasaki, K.; Kawasaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U03699; NID:9430718; PIDN:AAC13747.1; PID:9430719
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein
C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; F;536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>
F;538-674/Domain: flavodoxin homology <FEX>
F;538-674/Domain: flavodoxin homology <FEX>
F;197/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nitric-oxide synthase (EC 1.14.13.39) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;538-674/Domain: Llavodoxin nomolouy xrux
F;197/Binding site: heme iron (Cys) (axial ligand) #status predicted
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                                                                                                                                                                                                                             nitric-oxide synthase (EC 1.14.13.39) [similarity] - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68; DB 1;
Pred. No. 0.0099;
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Pred. No. 0.0099;
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R;Adachi, H.; Iida, S.; Oguchi, S.; Ohshima,
Eur. J. Biochem. 217, 37-43, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1147 <RES>
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72.28;
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72.28;
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                    25 NNNVEKTPGAIPSPTTQD
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S47647
nitric-oxide synthase (EC 1.14.13.39) - rat
cliptic-oxide synthase (EC 1.14.13.39) - rat
Cliptic-oxide synthase (EC 1.14.13.39) - rat
Cliptic Secies: Rattus norvegicus (Norway rat)
Cloate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Jun-2000
C.Accession: 847647; JC1472
Riceng, Y.; Almqvist, M.; Hansson, G.K.
Blochim, Blophys. Acta 1218, 421-424, 1994
A;Title: CDNA Cloning and expression of inducible nitric oxide synthase from rat vascule
A;Reference number: 847647; MUDD:94325351
A;Molecule type: mRNA
A;Residues: 1-1147 GEN>
A;Molecule type: mRNA
A;Residues: 1-1147 GEN>
A;Molecule type: mRNA
A;Reference number: JC1472; MUDD:919283; PIDN:CAA54208.1; PID:9439284
B;Nunokawa, Y.; Ishida, N.; Tanaka, S.
Blochem. Blophys. Res. Commun. 191, 89-94, 1993
A;Title: Cloning of inducible nitric oxide synthase in rat vascular smooth muscle cells.
A;Reference number: JC1472; MUDD:93191721
A;Accession: JC1472
A;Accession: JC1472
A;Accession: JC1472
A;Residues: 1-71, YY, 73-347, PVY, 350-678, VPV, 681-720, LY, 722-739, LY, 771-843, 'G', 845-10
A;Cross.references: DDM:D14051; NUD:9286560; PIDN:BAA03138.1; PID:9286261
A;Residues: 1-71, YY, 73-347, PVY, 350-678, VPV, 681-720, LY, 722-739, LY, 771-843, 'G', 845-10
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reductase homology; NADPH--ferrihemoprotein reductase homology CER>
F;338-674/Domain: NADPH--ferrihemoprotein reductase homology CER>
F;338-674/Domain: liavodoxin homology CELX>
F;338-674/Domain: ilavodoxin homology CELX>
F;338-674/Domain: flavodoxin homology (exial ligand) #status predicted
A;Title: Molecular cloning and expression of inducible nitric oxide synthase from human A;Reference number: A47475; MUID:93234523
A;Accession: A47475; MUID:93234523
A;Accession: A47475; MUID:93234523
A;Status: preliminary: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-422, 17,424-804,'D',806-830,'SP',833-932,'G',934-965,'A',967-986,'V',988-1
A;Residues: 1-422,'I',424-804,'D',806-830,'SP',833-932,'G',934-965,'A',967-986,'V',988-1
A;Residues: 1-422,'I',424-804,'D',806-830,'SP',833-932,'G',934-965,'A',967-986,'V',988-1
A;Residues: 1-422,'I',424-804,'D',806-830,'SP',833-932,'G',934-965,'A',967-986,'V',988-1
A;Residues: 1-422,'I',424-804,'D',806-830,'SP',833-932,'G',934-965,'A',967-986,'V',988-1
A;Residues: 1-422,'I',424-804,'D',806-830,'SP',833-932,'G',934-965,'A',967-986,'V',988-1
A;Residues: 1-422,'I',424-804,'D',806-830,'SP',833-932,'G',934-965,'A',967-986,'V',988-1
A;Residues: 1-422,'I',424-804,'D',806-830,'SP',833-932,'G',934-965,'Residue: Calalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH A;Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH A;Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH A;Description: catalyzes the oxidation fature predicted C;Reywords: calmodulin binding status predicted F;503-527/Region: calmodulin binding status predicted F;533-1127/Domain: NADPH-ferrihomoprotein reductase homology <FRH>F;531-1127/Domain: NADPP-radonine binding status predicted F;765-778/Region: PAD-Pyrophosphate binding status predicted F;765-778/Region: NADP-radonine binding status predicted F;765-778/Region: NADP-radonine binding status predicted F;700/Binding site: heme iron (Cys) (axial ligand) #status predicted
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Pred. No. 0.0099;
0; Mismatches 5; Indels
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Pred. No. 1.3e-05;
Mismatches 1; Indels
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72.28;
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Best Local Similarity 94.4%;
Matches 17; Conservative
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Best Local Similarity
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Rytausumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa Biol. Pharm. Bull. 19, 1374-1376, 1996
A;Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, an A;Reference number: US5027; MUID:97070590
A;Accession: UC5028
A;Accession: Jc5028
A;Accession: Jc5028
A;Reference number: Total Sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1147 <TSU>
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C; Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 04-Mar-2000
C; Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 04-Mar-2000
C; Accession: JG5097
R; Tsutsumishita, Y:; Kawai, Y:; Takahara, H:; Onda, T:; Miyoshi, J:; Futaki, S:; Niwa Biol. Pharm: Bull. 19, 1374-1376, 1996
A; Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, an kReference number: JG5027; MUID: 97070590
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A Exeridues: 1-1147 cTSU>
A Experimental source: uterus
C; Comment: This protein synthesizes nitric oxide from L-arginine.
C; Comment: This protein synthase; flavodoxin homology; NADPH--ferrihemoprotein re
C; Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me
F; 536-1124/nomain: NADPH--ferrihemoprotein reductase homology cFEH>
F; 538-674/Domain: flavodoxin homology cFEH>
F; 538-674/Domain: flavodoxin homology cFEH>
F; 538-674/Domain: flavodoxin homology cFEH>
F; 5497/Binding site: heme iron (Cys) (axial ligand) #status predicted
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C; Comment: This protein synthesizes nitric oxide from L-arginine.
C; Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein
C; Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FNN; heme; iron; 1
F; 536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>-
F; 538-674/Domain: flavodoxin homology <FLX>-
F; 197/Binding site: heme iron (Cys) (axial ligand) #status predicted
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                                                                                                                                                                                            nitric-oxide synthase (EC 1.14.13.39) L - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan.1997 #sequence_revision 31-Jan-1997 #text_change 04-Mar-2000
C;Accession: JC5028
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A;Status: nucleic acid sequence not shown
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25 NNNVEKTPGAIPSPTTQD 42
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Matches 13; Conserv
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R; Tsutsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa, M. Biol. Pharm. Bull. 19, 134-1376, 1996
A; Tsutsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa, M. Biol. Pharm. Bull. 19, 134-1376, 1996
A; Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and u. A; Reference number: JC5027; MUID:97070590
A; Reference number: JC5027
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-1147 <TSU>A; Residues: 1-1147 <TSU>A; Residues: 1-1147 <TSU>A; Residues: 1-1147 <TSU>A; Residues: 1-1147 <TSU
A; Residues: 1
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R; Karlsen, A.E.; Andersen, H.U.; Vissing, H.; Larsen, P.M.; Fey, S.J.; Cuartero, B.G.; M Diabetes 44, 753-758, 1995
A; Title: Cloning and expression of cytokine-inducible nitric oxide synthase cDNA from ra A; Reference number: 153165; MUID:95309542
A; Accession: 151165
A; Accession: 151165
A; Accession: 151165
A; Accession: 151165
A; Reference number: 153165; MUID:9886072; PIDN:AAA85861.1; PID:9886073
A; Residues: 1-1147 <RES>
A; Residues: 1-1147 <RES>
A; Cross-references: EMBL:026686; NID:9886072; PIDN:AAA85861.1; PID:9886073
C; Genetics: A; Genetics: C; Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reducce; Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal F; 536-11247/Domain: NADPH--ferrihemoprotein reductase homology <FEH>
F; 536-11247/Domain: flavodoxin homology <FLX>
F; 197/Binding site: heme iron (Cys) (axial ligand) #status predicted
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
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C.Species: Rattus norvegicus (Norway rat)
C.Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 20-Jun-2000
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Pred. No. 0.0099;
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Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                    25 NNNVEKTPGAIPSPTTQD 42
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A.Residues: 1-758 <a href="Yest-dues">1-758 <a href="Yest-dues">1-758 <a href="Yest-dues">Yest-dues</a>: 1-758 <a href="Yest-dues">Yest-dues</a>: 1-758 <a href="Yest-dues">Yest-dues</a>: Yest-dues</a>: Residues: Expussion No. Septembers (AB972)</a>
A.Purnelle, B.; Comblez, S.; Coster, F.; Naveau, F.; Goffeau, A. Submitted to the EMBL Data Library, March 1996
A.Pescription: The sequence of 55 kb on the left arm of yeast chromosome XVI identifit ogue to the human phosphotyrosyl phosphatase activator PTPA and a homologue to the plant A.Reference number: S69428
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N;Alternate names: hypothetical protein s110227
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S74559
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                              chromoprotein; FAD; flavoprotein; FMN; heme; iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein YPL158c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein P2570
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 05-Dec-1997
C;Accession: S65169; S6941
R;Purnelle, B.; Coster, F.; Goffeau, A.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S65154
A;Reference number: S65169
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                   C; Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FNN F;506-535 Fregion: Calmodulin binding F;536-1124 /Domain: NaDPH--terithemoprotein reductase homology <FEH>F;536-1124 /Domain: NaDPH--terithemoprotein reductase homology <FEH>F;538-674 /Domain: flavodoxin homology <FEX>F;539-618 /Region: blopterin binding F;539-618 /Region: blopterin binding F;54-75 /Region: FAD binding #status predicted F;764-775 /Region: FAD binding #status predicted F;961-910 /Region: FAD binding #status predicted F;1074-1087 /Region: NADPH binding #status predicted
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Pred. No. 1.2;
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Pred. No. 14;
3; Mismatches
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61.1%;
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Matches 11; Conservative
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309 NVQKVPSATNSKTTK 323
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R:X1e, Q.; Cho, H.J.; Calaycay, J.; Numford, R.A.; Swiderek, K.M.; Lee, T.D.; Ding, A.; Schere 256, 252-228, 1922
A:Thier Cloning and characterization of inducible nitric oxide synthase from mouse macr A:Recension: A4371
A:Stetus; Perliminary
A:Retus; Perliminary of compared with conceptual translation
A:Retus; Perliminary of Compared With Conceptual
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
C;Accession: 565440
Ex;Iwashina, M.; Hirata, Y.; Imai, T.; Sato, K.; Marumo, F.
Bur. J. Blochem. 237, 668-673, 1996
A;Title: Molecular cloning of endothelial, inducible nitric oxide synthase gene in A;Reference number: 565440; MUID:96235231
A;Accession: 565440
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 23-Mar-2001
C;Accession: T16057
R;Pulton, L.
Submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F13D11.
A;Reference number: S69020
A;Accession: T16057
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Genetics:
A;Cross-references: EMBL:U40939; NID:g1072175; PID:g1072177; PIDN:AAA81701.1; CESP:F13D1
C;Genetics:
A;Gene: CESP:F13D11.2
                                         A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Molec
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A:Introns: 31/3; 46/1; 76/1; 92/1; 118/1; 156/1; 194/2; 287/3; 332/3; 347/1; 385/1
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Pred. No. 10;
4; Mismatches 2; Indels
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Pred. No. 53;
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170 DPGPTASSSPLTQD 183
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A; Accession: S74559
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hunchback-related protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T43676
R;Fay, D.S.; Stanley, H.M.; Han, M.; Wood, W.B.
Dev. Biol. 205, 240-253, 1999
A;Title: A Caenorhabditis elegans homologue of hunchback is required for late stages
A;Reference number: 222622; MUID:99117349
ä
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A;Cross-references: EMBL:AF097737; NID:g4323034; PIDN:AAD16170.1; PID:g4323035 C;Genetics:
A;Gene: hbl-1
  Gaps
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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                                                                        189 NNNNEEAPASTVSACSTPTT 208
                                              1 NNNVEKAP----SATSSPVT 16
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  Conservative
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cencore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM protein - protein search, using sw model	<pre>Run on: September 10, 2001, 14:00:25; Search time 67.08 Seconds (without alignments) 16.268 Million cell updates/sec</pre>
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Title: Perfect score: Sequence:	US-08-833-506C-32 91 1 NNNVEKAPSATSSPVTQD 18
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	412676 seqs, 60623988 residues

412676 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 08 Maximum Match 1008

A_Geneseq_0601:* 9... 111... 112... 112... 114... 116... 119... 119... Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Human iNOS peptide Human iNOS peptide Human iNOS (25-42) Human iNOS peptide Inducible nitric o Sequence encoded b Nitric-oxide-synth Hepatocyte inducib Amino acid sequenc Human inducible ni Human inducible ni Description AAW81175 AAW81277 AAW96322 AAR55764 AAR63206 AAR8464 AAW36113 AAW361124 AAW81207 AAW81211 П DB Query Match Length 18 18 18 18 1146 11153 11153 11153 1000.0 1000.0 944.5 944.5 944.5 944.5 944.5 944.5 945.5 Score 91 91 91 86 86 86 86 86 86 86 10 10 10 11 10 Result 8

Human iNOS peptide		Human iNOS peptide	Human iNOS peptide	Rat 1NOS (25-42) p	Human 1NOS peptide	Rat iNOS peptide f	Rat inducible nitr	Human iNOS peptide	Mouse inos peptide	Human iNOS peptide	Human iNOS peptide	Human iNOS peptide	Human iNOS peptide	Mouse iNOS (25-42)	Inducible nitrogen	Inducible nitric o		Human 1NOS peptide	Human iNOS peptide	inos		Amino acid sequenc	Amino acid sequenc	Amino acid sequenc	Amino acid sequenc	Human BRCA2 tumour	Human secreted pro	Human secreted pro	Chimeric endogluca	Chimeric endogluca	fySSRP. Saccharom	S. cerevisiae SSRP	DESTINATION VINE NEW DESTINATION
AAW81218	AAW81284	AAW81280	AAW81214	AAW81177	AAW81321	AAW81213	AAW02571	AAW81320	AAW81212	AAW81219	AAW81285	AAW81281	AAW81215	AAW81176	AAR77360	AAW51246	AAW81220	AAW81286	AAW81216	AAW81282	AAB08720	AAB08719	AAB08721	AAB08722	AAB08715	AAY56029	AAG01517	AAY76149	AAW04936	AAW04935	AAR38746	AAW39214	AAB42125
19	19	19	19	19	19	19	17	19	19	19	19	19	19	19	16	19	19	19	19	19	21	21	21	21	21	21	21	21	17	17	14	19	21
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82.4	82.4	80.2	80.2	74.7	74.7	74.7	74.7	68.1	œ	ഗ	62.9	4	4	62.6	62.6	62.6	51.6	51.6	48.4	48.4	48.4	48.4	48.4	48.4	48.4	47.8	45.1	45.1	45.1	45.1	45.1	45.1	45.1
75	75	73	73	68	68	68	68	62	62	9	9	59	59	57	57	57	47	47	44	44	44	44	44	44	44	43.5	41	41	41	41	41	41	4.1
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	. 32	33	34	32	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT

Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis; Mab. Human iNOS peptide fragment capable of binding Mab 21C10-1D10 #1. AAW81207 standard; peptide; 18 AA. 30-APR-1999 (first entry) Homo sapiens WO9845710-A1 15-0CT-1998 AAW81207; AAW81207 

97WO-US06500 97US-6667777 (WEBB/) WEBBER R. 11-APR-1997; 07-APR-1997; Webber R;

Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics. WPI; 1998-594495/50

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                                                       specific bidding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (inds) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.
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                                            invention describes an immunoassay method where a sample with a
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Pred. No. 1.5e-07;
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             Example 3; Page 32; 93pp; English
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                                                                                                                                                                                                                                                                              100.0%;
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tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psorlasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inducible nitric oxide synthase; INOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.
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100.0%; Pred. No. 1.5e-07;
Live 0; Mismatches 0;
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Pred. No. 8.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.5%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-US06500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NNNVEKAPSATSSPVTQD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 nnnvekapsatsspvtgd 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-594495/50.
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Matches

AAW81277

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chemoattractant protéin-1. The methods can be used for the treatment of e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity, wasting syndromes, short stature, osteoporosis, inflammatory
                                                                                                                    diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell; fatty acid; lipotoxic; cytotoxic; cytokine; osteoporosis; inflammatory disease; autoimmune disease; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protection of mammalian cells against immunotoxicity or lipotoxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                achieved by blocking free radical memoration of free radicals in that cell. Treatment of insulin dependent diabetes mellitus (IDDM) can be achieved by by blocking nitric oxide (NO) production in a pancreatic beta cell and by providing a composition comprising an agent that reduces levels of fatty acids in the cells and protects beta cells of the subject against lipid-mediated cell death. Cells can also be protected against lipid-mediated cell death. Cells can also be protected against intric oxide mediated cytotoxicity by introducing into the cell an antioxidising agent. The methods can be used for protecting cells against immunotoxicity mediated by, e. g. 1L-1 beta. 1L-1 alpha, agamma IFN, TNF alpha, granulocyte-macrophage colony stimulating factor or monocyte

    used for treating, e.g. diabetes, obesity, wasting syndromes,
osteoporosis, inflammatory diseases, autoimmune diseases or

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibition of cytokine mediated immunotoxicity of cells can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86; DB 20; Length 1146;
Pred. No. 0.0001;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases, or neurodegenerative diseases
                                                                                                   Manganese containing superoxide dismutase; MnSOD; IDDM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newgard CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koyama K, Lee Y, Newg
, Thigpen A, Unger RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 247-251; 253pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR55764 standard; Protein; 1153 AA.
                                                              Inducible nitric oxide synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.58;
94.48;
                                                                                                                                                                                                                                                                                                                         98WO-US15781
                                                                                                                                                                                                                                                                                                                                                            98US-0055092
97US-0055092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurodegenerative diseases
                      28-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        (BETA-) BETAGENE INC.
(TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hohmeier H, Ka
Shimabukurom,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11111111 | 111111111 | 25 nnnvekapcatsspytgd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-153448/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX08434
                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                          W09906059-A2
                                                                                                                                                                                                                                                                                                                       30-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                   30-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                              03-MAR-1998;
                                                                                                                                                                                                                                                                                 11-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohneda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR55764;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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ID AAR5
XX
AC AAR5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (1NOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                       nitric oxide synthase; iNOS; human; immunoassay; detection; antibody; mimic; quantitation; sepsis; septic shock; lupus; infarction; tissue rejection; transplantation; psoriasis;
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 86; DB 19; L. Pred. No. 8.8e-07; 1; Mismatches 0;
    1;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune disease; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW96322 standard; Protein; 1146 AA.
                                                                                                                                                                                    AA.
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                                                                                                                                                                                                                                                                                                    Human iNOS peptide fragment #3.
                                                                                                                                                                              AAW81277 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.5%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US06500
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                                                              1 nnnvekapcatsspvtgd 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NNNVEKAPSATSSPVTQD 18
                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 94.5
Best Local Similarity 94.4
Matches 17; Conservative
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-594495/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WEBB/) WEBBER
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9845710-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-APR-1997;
                                                                                                                                                                                                                                                             30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1998
17;
                                                                                                                                                                                                                                                                                                                                            Inducible;
                                                                                                                                                                                                                                                                                                                                                                monoclonal
                                                                                                                                                                                                                                                                                                                                                                                   myocardial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Webber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Invention
                                                                                                                                                                                                                       AAW81277;
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AAW96322

us-08-833-506c-32.rag

(first entry)

28-DEC-1994

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nitric-oxide-synthase. cDNA was generated and used to construct a library in lambda ZAPII. This was screened with a 650 bp fragment of mouse inducible NO-synthase cDNA to identify the full-length clone pBSHSINOS. The insert was transferred to pSVL to give a vector capable of expressing NO-synthase in CHO cells under control of a heterologous constitutive promoter.
                                                                                                                                                                                                                                                                                                     Human chondrocytes were incubated with interleukin-1-beta to induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An inducible nitric oxide syntase (iNOS - AAR88464) is the product
                                                                                                                                                                                                            for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inducible nitric oxide synthase; iNOS; hepatocyte; gene therapy; vascular occlusive disease; cancer; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inducible nitric oxide synthase gene - useful in gene therapy treat, e.g. vascular occlusive disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 15; Length 1153; 0.0001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                        New human inducible nitric oxide synthase - useful identifying enzyme inhibitors and stimulators, and and treatment of e.g. viral infections or tumours
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simmons RL,
                                                                                                         Moncada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 86; DB ]
Pred. No. 0.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatocyte inducible nitric oxide synthase.
                                                                                                       Palmer RMJ,
                                                                                                                                                                                                                                                                Disclosure; Page 25-31; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 54-58; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nussler AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR88464 standard; Protein; 1153 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.5%;
94.4%;
94WO-GB00621
                                 93GB-0006386
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                                                                    (WELL ) WELLCOME FOUND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NNNVEKAPSATSSPVTQD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nnnvekapcatsspvtgd 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 94.45
                                                                                                       Moncada SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Geller DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYPI-) UNIV PITTSBURGH
                                                                                                                                        WPI; 1994-333198/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-068641/07
                                                                                                                                                                                                                                                                                                                                                                                                                                             1153 AA;
                                                                                                                                                          N-PSDB; AAQ77700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT10115
25-MAR-1994;
                                 26-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUN-1995;
                                                                                                       Charles IG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR88464;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone pHINOS from lambda Zap II cDNA library. The original source was induced human hepatocyte RNA. HINOS cDNA plasmid is pref.
Lransformed in E. coli SOLK ARCC 69126). The inventors claim a clone with the cDNA sequence in AAQ66914 and a cDNA clone which encodes AAR55764. The cloning and expression of a human tissue nitric oxide synthase cDNA provides a source of the enzyme for therapeutic purposes, for example to prevent the hypotensive shock seen with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                         Sequence encoded by the cDNA clone for human hepatocyte inducible nitric oxide synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ66914 is from human hepatocyte inducible nitric oxide synthase
                                                                                                                                                                                                                                                                                                                                                                                                                         encoding human inducible nitric oxide synthase - used the hypotensive shock seen with sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interleukin-1-beta; pBSHSINOS; arthritis; hypertension;
septic shock; inflammation; ischemia; dementia; obesity; tumor;
agonist; antagonist; vector; CHO; Chinese hamster ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                 Nitric oxide synthase; hepatocyte; hypotensive shock; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 86; DB 15; Length 1153;
Pred. No. 0.0001;
); Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nitric-oxide-synthase; NO-synthase; NOS; chondrocyte;
                                                                                                                                                                                                                                                                                                                                      Simmons RL;
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Nussler AK,

Geller DA, PITTSBURGH

Billiar TR,

(UYPI-) UNIV

WPI; 1994-200273/24.

N-PSDB; AAQ66914

cDNA clone to prevent

93WO-US11401 92US-0981344

23-NOV-1993; 25-NOV-1992;

Homo sapiens

WO9412645-A.

09-JUN-1994

Disclosure; Fig 1; 53pp; English.

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Gaps

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AAR63206 standard; Protein; 1153 AA.

**AAR63206** 

(first entry)

09-MAY-1995

AAR63206;

Nitric-oxide-synthase.

cell culture

WO9423038-A.

HOMO

13-OCT-1994

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17; Conservative

Best Local Similarity Matches 17; Conserv

Query Match

1 NNNVEKAPSATSSPVTQD 18 nnnvekapcatsspvtgd 42

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94.5%;

1153 AA;

Sequence

sepsis.

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Query Match 94.5
Best Local Similarity 94.4
Matches 17; Conservative
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                                                                                                                                                                                        30-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                 09-JUL-1999;
09-JUL-1999;
                                                                                                                                                                                                                                                                                                                    18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          Vogels R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sednence
                                                                                                                                                                  AAB31724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                    10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB66724
                                                                                 QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This protein comprises human penis inducible nitric oxide synthetase (HPINOS). Its amino acid sequence was deduced from a compa clone (see AAT98199) derived from human penile smooth muscle cell mRNA. The invention is directed to a method of treating crectile dysfunction in a patient by providing an agent capable of treating erectile dysfunction, and introducing an effective amount of the agent into the penile tissue of the patient. Preferably, the agent into the penile tissue of the patient. Preferably, the NoS is iNOS, and the agent is introduced into the corpora cavernosa of the penis. The agent is introduced into the corpora cavernosa of the penis. The agent is preferably an NOS inducer, an NOS protein such as HPINOS, a cDNA transformed penile cells, especially corpora cavernosa
                                                                                                                               Gaps
of a cDNA clone (AAT10115) derived from human hepatocytes induced for iNOS biosynthesis. The iNOS can be obtd. by expression of the cDNA e.g., in mammalian host cells and is used in the development of selective inhibitors of NOS or to treat diseases affected by nitric oxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of erectile dysfunction - by introducing an agent into penile tissue, particularly for inducing cavernosal smooth muscle relaxation or increasing NOS levels
                                                                                                                                                                                                                                                                                                                                Nitric oxide synthetase; NOS; iNOS; HPINOS; human; erectile dysfunction; impotence; gene therapy; corpora cavernosa;
                                                                                                                              ;
0
                                                                                                        Score 86; DB 17; Length 1153; Pred. No. 0.0001;
                                                                                                                              1; Indels
                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                         Human inducible nitric oxide synthetase
                                                                                                                                                                                                                                     AAW36113 standard; Protein; 1153 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 38-41; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rajfer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GONZ/) GONZALEZ-CADAVID N F
                                                                                                        94.5%;
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                                                                                                                                                     1 NNNVEKAPSATSSPVTQD 18
                                                                                                                                                                  11-MAY-1998 (first entry)
                                                                                                      Query Match
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gonzalez-Cadavid NF,
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                                                                      1153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAJFER J.
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                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid delivery vehicle comprising a nucleic acid encoding nitric oxide synthase, used for isolated tissue perfusion treatment to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes a method for gene therapy for enhancing and inducing anglogenesis. The method uses a nucleic acid delivery vehicle, which comprises a nucleic acid encoding nitric oxide synthase (NOS). The delivery vehicle is used for the manufacture of a pharmaceutical composition for isolated tissue perfusion treatment. The method is useful for enhancing and/or inducing anglogenesis in patients with endothelial dysfunctions, in particular arteriosclerosis. The present sequence represents an inducible NOS.
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a human inducible nitric oxide synthase (NOS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene therapy, angiogenesis; nucleic acid delivery; arteriosclerosis; nitric oxide synthase; NOS; endothelial dysfunction.
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Score 86; DB 19; Length 1153; Pred. No. 0.0001;
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; Mismatches 1; Indels
                                                   1; Indels
                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                        AAB31724 standard; Protein; 1153 AA.
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94.5%;
94.4%;
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99US-0143101.
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                                                                                                       1 NNNVEKAPSATSSPVTQD 18
                                                                                                                                     1 NNNVEKAPSATSSPVTQD 18
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and induce anglogenesis
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(WEBB/) WEBBER
                      07-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
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                                                                                                  Webber
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                                                                                                                                                                                                                                                                                                                                                                                                                            Use of a nucleic acid delivery vehicle comprising a nucleic acid encoding nitric oxide synthase, especially useful in gene therapy for enhancing and/or inducing angiogenesis and treating atherosclerosis \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to use of a nucleic acid delivery vehicle comprising a nucleic acid encoding nitric oxide synthase (NOS) activity for the manufacture of a composition for essentially isolated tissue perfusion treatment to enhance and/or induce angliogenesis. The nucleic acid delivery vehicle is particularly useful in gene therapy for the treatment of atherosclerosis.
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                                                                            Nitric oxide synthase; NOS; angiogenesis; gene therapy.
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Pred. No. 0.0001;
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                                        Human inducible nitric oxide synthase.
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09-APR-2001 (first entry)
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                                                                                                                  Homo saptens
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This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autofimmune disease; multiple sclerosis; epitope mapping.
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                                                                                                                                                                                                                                                                               Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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100.0%; Pred. No. 3.3e-05;
ive 0; Mismatches 0;
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100.08; F1
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97US-6667777
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                                                                       (WEBB/) WEBBER R.
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represents a peptide from human iNOS which is used in the method of the
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Modified-site
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                     invention.
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                                                    This invention describes an immunoassay method where a sample with a specific binding entiry (e.g. a monoclonal antibody) reactive to human inductible nitric oxide synthase (iNOS) or mindcs of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in calls and tissues for various pathophysiclogical conditions such as sepsis, septic shock myocardial infarction, rejection of tissue in organs following such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; milic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis; epitope mapping.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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100.0%; Pred. No. 3.3e-05;
ive 0; Mismatches 0;
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                   4; Fig 7A; 93pp; English.
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                             15 AA;
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                                                                                                                                                                                                                                            nvention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW81280;
                                                                                                                                                                                                                                                                               Sequence
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This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autofimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autoimmune disease; multiple sclerosis.
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
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Pred. No.
                                                                                   Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human iNOS peptide fragment PS-5243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 AAW81214 standard; peptide; 15 AA.
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                                                                                   Query Match 80.2
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